

APPENDIX A: DNA SEQUENCES

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>RXA00734-downstream

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>RXA00759-upstream

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>RXA00759

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>RXA00950-upstream

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>RXA00980-upstream

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>RXA01000

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>RXA01002
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>RXA01012

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>RXA01013

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>RXA01972
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>RXA01972-downstream
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>RXA01986-upstream
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>RXA01986
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>RXA01995-upstream

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>RXA01995

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>RXA02033-upstream

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>RXA02033

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>RXA02033-downstream

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>RXA02034-upstream

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>RXA02034

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>RXA02035-upstream
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>RXA02035
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>RXA02062-upstream
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>RXA02062
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>RXA02062-downstream
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>RXA02068
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>RXA02079-upstream
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>RXA02079
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>RXA02079-downstream
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>RXA02096-upstream
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>RXA02096
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>RXA02119-upstream

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>RXA02119

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>RXA02119-downstream

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>RXA02220-upstream

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>RXA02220
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>RXA02222-upstream
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>RXA02222
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>RXA02312
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>RXA02313-upstream
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>RXA02313
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>RXA02344
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>RXA02348
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>RXA02353
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>RXA02354-upstream

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>RXA02354

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>RXA02394

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>RXA02402

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>RXA02422

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>RXA02438-upstream

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>RXA02438

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>RXA02439-upstream

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>RXA02439

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>RXA02441
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>RXA02442-upstream
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>RXA02442
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>RXA02447
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>RXA02451-upstream
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>RXA02451
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>RXA02491-upstream
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>RXA02491
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>RXA02507-upstream
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>RXA02507
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>RXN02549--downstream
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>RXN02614--upstream

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>RXN02925

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>RXN02933
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>RXN03020
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>RXN03080

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>RXN03108-upstream

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>RXN03129
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>RXN03164-upstream
CTTTTTTGCATCCAGATGCACAAAGCCGTGGCACAACGAGACAACTGAGCACAATGGC
TGTCATGGCATATCAACCAGCAGACAATCGCTATGACGAC

>RXN03164
ATGATCTACCGCAGGGTGGGAAATTCTGGGCTGAAGCTTCCGGCAATTTGCTTGGGCTG
TGGCACAACCTTCGGTGATGACAAGCCGCTTTCAACGCAGCGCAGCATTATTCACCGCGCG
TTTGATAGGGGAGTCACTCACTTCGATTTGGCTAATAACTATGGACCTCCAGCAGGTTCC

GCAGAGACCAACTTTGGCAGGATTTTGGCTGAGGATCTCAAAAAGCCACCGCGATGAGTTG
ATCATTTCTTCCAAGGCGGGTTGGGATATGTGGCCTGGACCTTATGGTTTTGGTGGTTCC
CGAAAGTATCTAGTGAGTTCCCTTGATCAGTCCCTGACTCGCCTCGGCTTGGATTACGTG
GATATTTTCTATCATCACCGCCCGGATCCAGATACTCCTTTGGAAGAAACCATGTACGCA
TTGCGTGACATTGTTGCGTCTGGAAAGGCTCTTTACGTGGGTATTTCTTCC'TACGGTCCA
GAGCTCACAGCGGAGGCGGCTGAGTTCATGGCGGAGGAGGGCTGCCCCGTTCTGATTTCAT
CAGCCAAGCTATTTCCATCATTAAATCGTTGGGTGGAGGAACCGGGCGATGACGGTGAGAAC
TTGTTGCAGTCAGCTGCCAACAATGGTCTTGGCGTCATTGCTTTCTCACCCTTGGCGCAG
GGCCTGCTCACGGACAAATATCTCGATGGAATTCCAGAGGGTTCCCGCGCCAGCCAGGGT
AAGTCCCTGTCTGAGGGCATGTTGAACGTGAACAATATTGATATGGTCCGCAAGCTCAAT
GACATCGCCCAGGAACGCGGGCAGTCACTTGCGCAGATGGCGCTTGCATGGGTGCTGCGC
GAGCAAAGAGAGTACGGCGCCGGATTACCG

>RXN03164-downstream
TGACCAGTGCATTGATTGGTGTCT

RXS00088 - coding Region

ATCGAAGACAACCACGGCACCGAAGGGATCTCCCTGCCAATCGAGGGCGTCGCTGCGACCGACAACCGC
GCATTGCAACTGCTTGATCGCTGGGGTGTAGAGCTCGTTGCAGCTCCACTTCAGCTGGTTCCATTTACC
GTTACGGGCTACACCGAAGAGGGCGGCGTCGCTAACCTTGGCTCCCACCGCGAGCCAGACCTGGAAGCA
CTTGCTGCTGCACAGCCTTCCCTGATCATCAACGGCCAGCGCTTCGCTCAGTACTACGATGACATCATT
GCCCTGAACCCCTGACGCAACCGTTGTTGAGCTAGACCCACGCGATGGCGAGCCACTTGACCAGGAGCTT
ATCCGCCAGGCTGAAACCCCTCGGTGAGATCTTCCGCGAAGAAGAAGATGCTGCAAAGATCGTTGCTGAT
TTCGAGTCCGCACTTGAGCGCGCTAAGACCGCATACGCGACAATCTCCGACCAGACCGTCATGGCAGTT
AACGTTTCCGGCGGAAACATTGGCTACATCGCTCCTTCCGTTGGACGCACCTACGGTCCAATCTTCGAC
CTGGTTGGACTCACCCAGCACTCGAGGTTGGCAACGCGTCCTCCGACCACGAGGGCGACGACATTAAC
GTCGAAGCAATCGCAGCTGCAAACCCAGACCTGATCCTGGTCATGGACCGCGATGGTGGCACCAGCACC
CGCAACGAAGCTGATTACGTTCCAGCAGAGCAGATCGTCTCCGACAATGAAGCACTGGCAAACGTCAAG
GCTGTCACCGACGGATACGTTTACTACGCACCTGCAGATACCTACACCAACGAAAACATCATCACCTAC
ACCGAGATCCTCAACGGCATGGCAGATATGTTGAGAAGGCAGCTCAG

RXS00088 - 3'-Region
TAGGGGATCGATCCCACACTGAC

RXS00372 - 5'-Region

GCAGACATTTCCATAAGTCTTGCGAAATGCGCCCATTCATGTAAAGATGTTATTTCTCCCCAAACAC
TCCTTAAAATTTCAAGAAGGGCCTTATTTTC

RXS00372 - coding Region

ATGTCTTCGAAGCACCCCTTTGAAGCGCACTGCCGTTACTGTTTTTGCACCTCGGCGCTTCCGCTGCTCTC
CTCGTGGCTTGCTCTGAACCTTCTGAGGACGTTTCCACCGCAGAGACCACCACTGCAAGCTCTTCCGCT
AACGCATCCGATGCAGCCGGTGAAAAAGTAACCATCACCGTCTACACCTCTGAGCCTGAGGAAAAGGTC
GATGAGATCAACAAGGCGTTCATGGAAGCCAACCCAGATATTGAGGTTGAGGTGTACCGCGCTGGTACT
GGCGATCTGACTGCTCGCATTAAGCTGAAAAGGCATCCGGTTCTATCGAGGCTGATGTGTTGTGGGCT
GCGGATGCTGCAACCTTTGAACTTATGCAGCACAGGGCGACCTTGCAGAGCTGGAAGATGTTGAGACT
TCCGACATCATTGAAGAGGCTCTGGATGCTGAGAACTTTTATGTAGGCACCCGCATCATCCCAACCGTG
ATTGCATACAACACTGAAGTTGTTGATCAGGCTGAGCTTCCCTACGTCCTTGGGCTGATCTGACTGATCCT
AAGTATGCAGGCCAACTGGTCATGCCGATCCAGCTGTGTCTGGTGTGTCAGCCTTCAATGCTTCTGTG
TGGAAGAACGACCCCTGCGCTTGGCGAAGCCTGGATCACCGCCTTGGGTGAAAACCAACCAATGATCGCT
CAGTCCAACGGCCCAACCTCCCAGGAGATCGCTGGCGGTGGCCACCCAGTGGGCATCGTGGTGGACTAC
TTGGTGGCGGACTTGGCTGCTGCTGGATCTCCAATCGACACCATCTACGCATCGGAGGGTTCTCCTTAC
ATCACTGAGCCTGCAGGTGTGTTGCTGATTCTGAAAAGAAGGAAGCAGCCGAGCGCTACATCAACTTC
CTGCTGTCTGTTGAAGGCCAGGAAATCGCAGTTGAGCAGGCATACCTGCCAGTGCGTGAAGATGTGCGGA
ACTCCAGAGGGGCACCCCGAGTTGGCTGACATCGAGCTCATGACCCCTGACCTGGAGGTTGTAACCGCT
GATAAGGCGGCTGCTGTTGAGTTCTTCCAAAACGCAATGAAC

RXS00372 - 3'-Region
TAGTTTTCTTATGCAGTTATCTC

RXS00453 - 5'-Region

TAGTGGGGCGTGAAAAAATAGCTCATTTAAGAGGAGAAGCAACCCCGTGGCGAAATTGCTATTTCAGGTT
GGGGCGATGGTCTATAATCGCAAGTGGATT

RXS00453 - coding Region

GTGATTTTCGGCATGGCTACTTATTTTGGCCATTGTTGGTGGTCTGGCCCTGACGATGCAGAAGGGGTTCT
AGTAACTCTTTCACTATTGAAGACACCCCTTCGATTGATGCCACTGTTTCTCTGGTTGAAAATTTCCCT
GATCAGACGAACCCGGTGACGGCCGCCGGAGTTAACGTGGTTTTCCAATCCCCGGAAGGAACACGCTT
GATGATCCTCAGATGATGACTGCGATGGATGCAGTCGTTGATTACATTGAGGACAATTTGCCTGATTTT
GGTGGGGGAGAGCGCTTCGGCAATCCTGTTGAGGTGTCTCCTGCGTTGGAAGAGATGGTCATCGAGCAG
ATGACCAGCATGGGGCTTCCTGAGGAAACCGCTGCAAAGGATGCTGCCAATCTGGCGGTGTTGAGCGAA
GACAAAACCATTTGGCTACACCTCTTTCAACATTGATGTTGAGGCCGAGAAATATGTGGAGCAAAAACAC
CGCGATGTGATCAACGAAGCGATGCAAATCGGTGAAGATTTAGGTGTCCGGGTGGAAGCCGGTGGACCT
GCTTTCGGTGATCCAATTGAGATTGAAACCACAGTGAGATCATCGGTATTGGCATCGCGTTCATCGTG
TTGATTTTCACCTTTGGTTCCTTGATTGCTGCAGGCTTGCTTTGATTACCGCGGTGATCGGCGTGGGC
ATTGGTGCCTGGCAATTGTGCTGGCCACGGCGTTTACTGATCTCAACAATGTGACTCCAGTGCTCGCA
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GGCGCGACGGTGATTATCGCGCTGGTAGCCCTCATATTGCGGATATCGGATTCCTCACGGCCATGGGT
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CTGCCTTCTGACTCCACCTCCAATATTGATACCACTCAGCGTCAGTCGGCTGATTTGATGGCAGAGGGC
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GCATTGCAGCCACTGATTGAGGCACAGGAGCCTGAAGAGGGCGAGTTCGATCGGGAGCAGGCGGCTCGT
TTTGCTACCTATATGTATGTCACCCAGACCTACAATTCCAACATCGATGTGAAGAATGCGCAGATCATC
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ACCCCTGAGTTGATGCACGTGCTGCGTGCGCAGGAAGCTCAGATTGAGGATGTTACGGGAACCTGAACCTG
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CTCGCTGTGGTGTGTTGGTTTGGCTATTTTCTCCTCATTCTGGTGTTCGGTTCCCTGCTTGTTCGGCTG
GTTGCTGGCCTTGGCTTCTTGTGCTGTGGGTGCGGCCTTCGGTGCGACGGTGTGTTGCTGGCAGGAG
GGCTTCGGTGCTTTGTGAACACCCCTGGTCCGCTGATTTTCTTCATGCCGATCTTCTCATCGGCGTG
ACCTTCGGTTTGGCCATGGACTATCAGGTGTTTCTTGTGACTCGCATGCGCGAGCACTACACCCACCAC
AATGGCAAGGGACAGCCTGGTTCCAAGTACACCCCGGTTGAGCAGTCAGTGATTGAAGGCTTCACGCAG
GGCTCCCGCGTGGTTACAGCAGCGGCACCTGATCATGATTGCCGTGTTGTTGGCGTTTATTGATCAGCCG
TTGCCATTTATTAAGATCTTCGGTTTCGCGTTGGGTGCGGGCGTGTTTTTTCGATGCTTTCTTCATTTCGC
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CGAATTCTGCCAAGTTTGACATTGAAGGCACCGCACTGGAGAAGGAATGGGAGGAGAAGCAGGCTGCA
CGT

RXS00453 - 3'-Region

TAGACTTGGCACCTATGTCAGAT

RXS00479 - 5'-Region

TAGATCCCAAGGCTCAAAATTTATTACTTAAACAAGTTGAGCAACTAGCCAGCCGCAAATCTTAGAACT
AACCTTTACGCCTTTAACGGAAGTGAATTTG

RXS00479 - coding Region

ATGTCTACTAGCATCACAAACAGAGAACAAGAAGAAATCTGGTCCTCCTCGCTTGATGAGAATCTTTCTG
CCCGCCTTGCTAATTTTAGTTTGGCTTGTTAGGAGCTGGAGTCGGCGGTCCTTATTTTGGCAAGGTTAGT
GAGGTCTCCTCCAACAGCCAGACCACATATCTGCCAGAATCTGCCGATGCCACTCAAGTACAGGAACAG
TTGGGAGATTTTACTGATTCTGAATCCATCCAGCCATTGTGTAATGGTCAGCGATGAACCTTAAACA
CAGCAAGACATCACACAACCTCAATGAAGTTGTTGCTGGGCTTTCAGAATTAGACATAGTTTCCGATGAA
GTCTCCCCTGCTATTCCATCCGAGGACGGCAGAGCTGTCCAAGTGTGTTGTCCTTCAATCCATCAGCG
GAGCTGACGGAAAGCGTCGAGAAGCTCTCTGAGACCTTGACCCAGCAAACGCCGGACTATGTGAGCACC
TATGTGACCGGACCGGCTGGGTTTACCGCTGATCTCAGCGCAGCTTTCGCGGGTATTGATGGGCTACTC
CTAGCAGTCGCCTTGGCTGCCGTCTTGTCACTTCTGTCATCGTCTATCGCTCCTTCACTTCTGCCATC
GCCGTGCTTGCCACCAGTTTGTGTTGCGCTGACTGTAGCTCTATTGGTGGTGTGGTGGCTAGCTAAGTGG
GACATCCTGCTGCTTTGCGGTCAGACTCAAGGCATCCTCTTCATTCTGGTCATTGGCGCCGCCACCGAC
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 CTTATTGATACCCTGCTCGTTCGCGCCTTCTTGGTGCCTGCTTTGTTCTACGACATCGGACCGAAAATC
 TGGTGGCCGTCAAAATTGTCCAATCAGAAATACCAGAAGCAGCCTCAGCTA

RXS00479 - 3'-Region
 TGACACACCAAAATTCGCCTCTC

RXS00654 - 5'-Region
 CAGCAATAGCGATTATTGCTTGATTGTGTGTTTTTAGATCTTCGGTCTCTTCACTCAACTGCTGTGAA
 GTGCCACCTGTTTGAAAGGCGAACACGATA

RXS00654 - coding Region
 GTGCTCGATATTTTGATTTACCCGGTGTCTGGAGTGATGAAGCTGTGGCACCTGCTTCTTCAACAACGTT
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 TATTGGGTGAGCAACAACCTGTGGACGCTCCTCCAAACAATCATCATGATGGTCAATTTTGGAAACGCAAA
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 AATCGCGAGCCGTCTCAAGAGGAC

RXS00654 - 3'-Region
 TGATGTTGTGGACCAATCGAGAT

RXS00758 - 5'-Region
 TTCAAGTTTGGCTGTGACTCATGTGCGACATAGTATTTCAATCACCGGATCCGCACGATTGCAAAATCC
 TGGGGAATATTACATAACAACGGAGGTCACTC

RXS00758 - coding Region
 ATGACTTTGAAGAAGTCTCTCGCTGTAACCACGGCGGCTGCACTTGCTTTGAGCCTTGCCGCTTGCTCG
 TCCGACTCCTCGTCCGACAGCTCCTCATCTCATCAGGCAGCGAAGGCGGCGACAACCTACGTCCTCGTC
 AACGGCACTGAGCCACAGAACCCGCTCGTCCCAGGCAACACCAACGAAGTAGGTGGCGGTGCGCATCGTC
 GACAGCATCTTCTCCGGCCTGGTCTACTACGACGTGACGGCTCCCCTGTCAACGATGTTGCAGAGTCC
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CCAGTTACCGCTGAGAGCTTTGTCAACGCATGGAACATAACGTAGCTAACAGCACGCTGTCCTCCTAC
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 ACCACCTTACCGCTCGAGCTCACCCAGCCTGAGTCCGACTTCCCACTGCGCCTGGGATACTCCGCATTTC
 TTCCCGCTTCTGAATCCGCATTTGACGACATGGACGCATTTCGGTGAGAACCCAATCGGCAACGGTCCA
 TACAAGCTCCAAGAGTGGAACCAACCAGGACGCCACCATCGTTCTTAACGCGGACTACACCGGTGGA
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 CTCTCCGACAACCTTGATGTGCTGGACGCTATCCCAGACTCCGCGTTCTCCTCCTTCGAGGACGAGCTC
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 TTCTCCGGCGAAGAAGGCGTGCTGCGTCGCCAGGCCATCTCCTTGGCCGTCAACCGCGACGAGATCACC
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 GACGAGATCAGCCCTTGGTCCGGCGAGTTCTCCATCTCCTACAACGCAGACGGTGGACACCAGGCATGG
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 TTCAAGTCCCTGCGTGACGATGTACCAACCGCACCATCAACGGCGCATTCGCAACCGGTGGCAGGCA
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 CCGCTATAACAAGCAGACAGGAAATCCTGCTCCAGGATCTCCAGCGATCCCAACTTGGTACTCCAAC
 GCAGTTGGTGGATACTCCACCAACGTGGACAACGTGGAATTCCAGTGGAACCTCGCAACCTGCGTACTAC
 CAGATCACCAAGAAC

RXS00758 - 3'-Region
 TAGTAGCTTCGCACCAACCCGCTC

RXS00912 - 5'-Region
 CCACACCTTTGAAAGGAGCTAAGCG

RXS00912 - coding Region
 ATGGACAACACCCTCTACACAGCAGGCCCTACAATCGCAGCTGCCTTTTTTCATGCTGTCGTTTCATCTTC
 ACCATCTACCGCATCATCGTCGGGCCCAACTCCATCGATCGCCTACTCGGCC'TGGACGGAACCGTCTCC
 ATGATTCAATGCTCCATGGCCACCTACATCTGCTGGACACTCGACACCACCGTCACCAACTTCATGATG
 GTCATCGCACTCTTAGGATTCATCAGCTCTGTATCCGTAGCCCGCTTCCGCAAGAGGGATGGTGCC

RXS00912 - 3'-Region
 TAAATGACCCTGCAACTATTCAC

RXS00932 - 5'-Region
 CCCAATTAATTTATGCACTTCGGTGAGGTTACTCACAAAGAGTAGCGTGCAAAGCCCAGCAATAAGGTG
 ATGTTTCAACGATTAGGTTACGGTAGGGGCC

RXS00932 - coding Region
 ATGACGCCACAGAACTTCACCGTTTTGTCAGCCCTTTTAGAAATGGGTACCTGGACCCTGCTGATCATC
 GGCATGATCTTAAAATACAGTGGAGTGACAGACGCCGTAACCCCTATTGCCGGCGGTATCCACGGCTTT
 GGCTTCTCTGTTTTGCAGCCATCACCATACCGGTGTGGATCAATAATAAGTGGACATTCCCGCAGGGT
 ATCGCAGGTTTGATCGTCTCTGTTATCCCGTGGGCTGCATTGCCATTTGCATTGTGGGCAGACAAGAAG
 GGCCTCGTTGCCGGCGGATGGCGCTTTTCAGATCCGTCCGAAAAGCCACACACTTTCTTTGACAAGATC
 TTGGCTCAATTGGTCAGGCACCCAATCCGATCCATTTAATTCTGCTGGTGATTATCGCCGTCGTCTTC
 TCTATCTTGCTGGCGATGGGACCACCTTATGATCCAGATGCCATCGCAAACACTGTGGAT

RXS00932 - 3'-Region
 TAAACAACAGCCTCCTTCACATG

RXS01346 - 5'-Region
 AAGGTGTGGTGAGTCACTGGCTAGATTTGATTTGTTGGCCATACCAAATCGGCCCCACACAGGCACGTTG
 CAAACAGCAACGCTCACCCATAGGAGATTTA

RXS01346 - coding Region
 ATGCGCACAGCCACAAAAGTCATCGCAACAGTGATGGCCTCAACCCTGGCTATCGGGCTGGCATCTTGT
 TCCAGCTCTAGTGGCACCCAGAGCTGAATTACGTATCCGTCAACGGCACCGAACCTCAGCGCGGACTC
 ATCCCGGGCGACACCAATGAAAACGGCGGTGGGCGAGTGGTGGACATGCTGTACTCTGGGCTCGTCTAC
 TTTGATGAAGCTGGCGTTGCTCAAAATGACCTGGCGGCATCAATTGACCAGGAAACAGACACCACCTAC
 AAAATCACTTTGCGTGATGGCATCAAATTCAGTGACGGATCGGATATTACTGCCACTGATTTTGTGGAT

ACCTGGAATTTTGTAGTGAAAAATGGACTGCTCAACACTTCTTTCTCTCACCGATTAAAGGGTATGAG
 GAGGGCGTGAAACGCTCGAGGGTTTGAATGTGGTGGATGATCGCACATTTACCATCGAGCTTGCCCAA
 CCGGATTTCTGAGTTCACCCACGCATTGGCTACTACGGTTTTGCACCGATGCCAGCTTCGGCTCGCGAT
 GATATTGACGCCTTTGGTGAAAACCCCGTGTCTCTGGCCCTTACAACTAGAGCAGTGGGATCACAAC
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 TACGTGTTCTACGCCCCAAAATGATGCAGCTTATTAGATCTGTTGGCTGGAAACCTAGATGTGCTGGAT
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 CGACAAGCAATTTCTATGGCGATTAAACCGTGAAGAAAATCGCTGAGCAGATCTTCGCCGGCACCTACACG
 CCTGCGCTCGACTTCACCGCGCCCGTGTCTCGACGGCTGGCGCGATGATTGAACGGCAATGACGTGCTG
 ACTTTCAGCCTGACAAGGCCCGTGAAGTGTGGGAAGACGCTGAGGAGATCGCACCTTTTGAGGGCGAA
 TTGCAGATCCGATGACAAACGCGGATGTTCCCAACCGGAATGGGTGGATGCGGTAGCAAAACAGTCCAGC
 AACGAATTAGACGTCAACGCCACTGGCAATCCTTTCCCGATTTTAAATCCTTCGCGACACATACCGC
 ACCACCGGATTGGATGGCGCCTACCGCACCGCGTGGTTTGGCGACTACCCAAGCATCGGCAACTTCCTT
 GGACCTAACTACACCTCGGGCGTGGCCTCCAACGATGCCAAGTACGAAAACCCAGAATTTGATCAATTG
 ATTGCCGACGCCGAGCAGCCTCCACCAAGGAGGAAACCTTCCAGGCATATGCGCAGGCCCAGGAAATG
 TTGTTGCGCGATCTTCCCGCAATCCCACTGTGGTACCCGAATGTGGTTGGCGGCTACTCAGAATCCGTG
 GACAACGTCTCCGTAAACTGGAAGGCCATACCTGTTTATTGGGCAATTACAAAGCAA

RXS01346 - 3'-Region
 TAAACTCATTAACCTAAATCCGG

RXS01425 - 5'-Region
 AGTCCCTATTAATCCCAAGGAGTTTCGACTCACAGTGCTCAATTTTATTATTGGCCAATTTTCGGCCAT
 TCTGTGGTTCTGGCATAAAGCGTTTCAGCTTT

RXS01425 - coding Region
 GTGCTGAGCCAGATTCCGGAATTACCTGGGCTTGTGCGATCATGTTCTTGACCTTCACCGTGCGTATG
 GTTCTGGTCAAGCCGATGGTCAACACCATGCGTTTCACAGCGCAAGATGCAAGACATGGCTCCAAAGATG
 CAGGCCATCCGCGAGAAGTACAAAAATGACCAGCAGAAGATGATGGAGGAGACCCGCAAACTTCAAAAA
 GAAGTGGGCGTTAACCCCATCGCAGGCTGTTTGCCAATGTTGGTGCAGATCCAGTGTTCTCTGGGTCTG
 TTCCACGTGCTGCGCTCCTTCAACCGCACCGGTTCTGGCGTTGGCCAGCTGGAAATGACCGTTGAGCAA
 AACGCGAACACCCCGAACTACATCTTCGGTGTGACGAGGTTTCAGTCCTTCTGCGTGCAGACCTGTTT
 GGTGCGCCACTGTCGTCTACATCACCATGCCTGCTGACGCGTTCGACGCGTTCCTTGGCCTGGATGTC
 TCCCGCCTCAACATCGCGCTGGTTGCAGCTCCAATGATTTTGATCATTTGTCGTGGCAACTCACATGAAC
 GCGCGTCTGTCCGTCAACCGCCAGGAAGCTCGCAAGGCAGCCGGCAAGCAGCAGGCCGCTTCCAGCGAT
 CAGATGGCCATGCAGATGCAAATGATGAACAAGATGATGCTCTGGTTTCATGCCAGCCACCATTTTGTTC
 ACCGCTTCATCTGGACCATCGGTCTTCTTGTCTACATGATGTCCAACAACGTGTGGACCTTCTTCCAG
 CAGCGTACATCTTCGCCAAGATGGACGCTGAGGAAGCAGCTGAGGAGGAGGAAAAGCGCGCAGCAAAG
 CGCACTACCGCTCCAAAGCCTGGCGTGAAGCCAGAAAACCCCAAGAAGCGTAAGAAG

RXS01425 - 3'-Region
 TAAAACTTCACTAAAAACCGCCA

RXS01658 - coding Region
 GATCCACAGATCCTGTACCAACCTTCACCCAGCAACAGCAGCTGCGAACTTCTACGGTTTCCAGAGC
 CAGCTGGCGATGGACCGCTTTGAAGTAGATGGCAAACCTCCGCGACTTTGTTGTGGCAGCACGTGAGCTC
 GATCCAAACGCCCTGCAGCAAAACCAGCAGGACTGGATTAACCGTCACACTGTTTATACCCACGGCAAC
 GGCTTCATTGCAGCTCAAGCAAACAGGTGGATGAGGTGCGCCGCGACGTCGGATCCACTCGTGGTGGT
 TACCCTGTCTACACCGTCTCTGATTTGCAGTCGAATGCTCGTGTGCTGCAGAAAGCGAAGATGCTGAGGAG
 CTTGGCATCAAGGTTGATGAGCCTCGTGTGTACTACGGACCACTGATTGCTTCTGCGACTGATGGTGCT
 GACTACGCAATTGTGCGTGACACCGCGATGGCCAGTCGAGTACGACACTGACACCTCCAGCTACACC
 TACGAAGGTGCTGGCGGCGTGGACATTGGAACATGGTCAACCGTGCGATGTTTGCATTGCGCTACCAG
 GAAATGAACATGCTCCTGTCTGATCGTGTGGTTCCGAATCCAAGATCCTATTTGAGCGCGATCCTCGT
 TCCCGTGTGGAAGAGTTGCACCTTGGTTGACCACTGACTCCAAGACCTACCCAACCTGTGATTGATGGT
 CGCATCAAGTGGATCGTCGATGGCTACACCACCTTGGATAGTCTTCCGTACTCCACGCGACCTCACTG
 ACGGAAGCGACTCAGGATGCTGTATGCCTGACGGCACCCACAGCCACTGATCACAGATAGGGTGGT
 TACATCCGCAACTCCGTGAAGGCTGTTGTTGATGCGTACGACGGAACGTTGAACCTTACGAATTTCGAC
 ACCGAAGATCCTGTTCTGAAGGCATGGCGTGGCGTGTTCAGACACCGTGAAGGACGGGTGCGGAGATT
 TCCGATGAGCTTCGCGCACACCTGCGTTACCCAGAAGATTTGTTCAAGGTCCAGCGTGACATGCTGGCC
 AAGTACAACGTTGATGATTCTGGAACATTCTTACCAACGATGCGTCTGTTCTGCTCCAGGTGACCCA

ACTGCAGCGGAGGGCCGCCAGGAACCTTAAGCAGCCTCCTTACTACGTGGTGGCAGCAGACCCAGAGACC
GGTGAGTCCAGCTTCCAGCTGATCACCCCGTTCCGTGGACTTCAGCGCGAGTACCTCTCTGCACACATG
TCTGCGTCTGCTGATCCAGTTACCTACGGTGAATCACTGTTTCGTGTGCTGCCTACCGATTCTGTGACC
CAGGGTCCAAAGCAGGCCCAGGATGCGATGATGTCATCTGACCAGGTTGCTCAGGACCAAACACTGTGG
CGTGGATCGAACGATCTGCACAACGGAACCTGTTGACCTTGCCAGTTGGTGGCGGAGAGATCCTCTAC
GTTGAGCCGATTTACTCGCAGCGCAAGGATCAGGCATCGGCCTTCCCGAAGCTTCTGCGCGTGTGGTC
TTCTACAAGGGTCAGGTTGGTTACGCACCAACGATCGCTGAAGCCCTATCGCAGGTCGGCATTGATCCG
AAGGAAGCGCAGGACATCGAAGAGGTAGATGGCACCCTACGACGCCATCGACTGATGAGACTGACACT
GACACTGATCAGCCTGCAACCGAAACCCCAACTGCACCAGTGAGTGAGGCGGAAGGAATCGCGGCCATC
AACGATGCGTTGAGCAACCTTGAAGCTGCTCGCGATAGCTCTTTCGAAGAGTATGGTCGTGCACTCGAT
GCGCTTGATCGTGCCGTCGATAGCTACCAGTCCGCACAG

RXS01658 - 3'-Region
TAGCGTTTGAGTAAACAGCCCGA

RXS01677 - 5'-Region
GTCGCCATAGTTGAGTTTTATTTCATGGCTTTTAGCTAGGCGACTTTAGTTGAGGGCTTTTAGTTGAGGG
CTTCCCAGCAGGGATGGTTAAGGAGAATTCA

RXS01677 - coding Region
GTGAACCAACAGAGTAAAAAGTGGCTCGTACCGACACTGGTCGTATCATTGCAGTGCTCCTCATCGCA
GTTGTTCTGTTGATGTACCGAGGAAATGCGAGTGATACGGCCGAGGGCGTTTCAGCCGCTGCGACTTCG
GACTCGGCTGCTGCTTCGACTGCTGCTTCGGGTTCCGCTTCTGGTGTGCGGACTCCGATCTGACCAGC
GTGGAAGCACGCGACCCCTTCGACCCCTGTTGCGGTGGGAGACGTTGATGCACCTGTTGGGTAGTGGTG
TTTTCCGACTACCAATGCCCCGTTCTGTGCAAAGTGGAGCGATGAAACCCGCCACAGATGATGAAGCAT
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GCTCGCGCGGCATACGCTGCGGGTTTGAGGACGCATACTTGGAATACCACAACGCACTCTTTGCCAAC
GGTGAAAAACCCAGCGAAGACCTGCTCAGCGAAGAGGGACTTATTAAGCTTGCTGGTGACCTTGACTA
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CTGGGAATCGATCTTGCGCCTACTCCACCCAGCTTTCTCTAGGTGGCCAGCCAATCATGGGCGCT
CAGCCTGCTTCTGTATTTGAAGCCGCTTCGAGCAAGCACTGGCAGCGAAAGAA

RXS01677 - 3'-Region
TAAACCGTGGATGTCGGCCTAGT

RXS02586 - 5'-Region
TTCTCTGAGATCGTCATGATGAAGTACATCGCGTTCGGCATGATCGCAGCGCTGATTCTGGATGCCACC
ATCATCCGCATGCTGCTTGTCCTCCCGCCGCTG

RXS02586 - coding Region
ATGCACCTGCTTCGCGACGACAACCTGGTGGGCACCCGGCTTCGTTAAAAAGGCCCTACACCGTCATGGGT
CACGGCTCTGAGGTGGAGGAAGCACCTCGCCCAACACCCGTCGCCTCAACGACGATGAGGAAGTCACC
GTGCATGAAGCAGTTGTGCTGGCGATACCGTGGCATCTCGCGGTGGTTTGAGCACGCAGGAAAACCGT
GATCTGGTGTCTTCGTGGAACCTAAGGCTCGTTTGAAAAGCGCAGGCTTGAGGATCTAGAT

RXS02586 - 3'-Region
TAAATCTATGCGAGGATTTTCA

RXS02587 - 5'-Region
AGCCTGGATAACCTGCCAGACGGTGGCGCATGGCTGCAGCGCTTCGCCCTCTGACTGCCTTGTTATCC
AACCGCCACAATTCCCAGGAGTAATCCACCC

RXS02587 - coding Region
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ATTTTGCTTTGTTTGTGATTTTCGGCACCAAGCTGGGCGACCGCATGAGCCAGGAAGGATGGGATGAT
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GTCGTGTTGCTGTTTACTGCGCCTGAAGGCACTTTTCGATGATGCAGAGGTGTTCTCCAGCATCTCT
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CGTAATCAAAATCTCCTCAGCAAAGACGGCACCCAAACCTTTGCAGCTCTCGGGCTCAAAGGTGACGGC
GAGCAAACGCTGAAGGACTTCCGGGAGATTGAAGATCAGCTCCATCCGACAACTTGCCGGTGGCGTC
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 GCTGCTTTGATGTCGGTGACGGTGTGGCGTCTGCTGTTTCAGCATGTTGGGTAAGAATATCGATAAGTGG
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 CTGGGTATGGGTGCCACCTTGGGTATTCTCACCTTGATGTTTCGTCGATGGCGTGGGTGCCAGCGCATTG
 AACTTCTCCCTTGCCCACTGATGAGTCCAGTGCTGGTGCTGATCATGGCTATTATTTACGGACTTTCC
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 GCCATCAGATACGGCACTGCACACACCGGATCTATCATCACCGCGCGCCGCACTGATCATGATTGTGGTC
 TGTGGAGCGTTTGGTTTCTCTGAGATCGTCATGATGAAGTACATCGCGTTTCGGCATGATCGCAGCGCTG
 ATTCTGGATGCCACCATCATCCGCATGCTGCTTGTCCCCCGCCGTGATGCACCTGCTTCGCGACGACAA
 CTGGTGGGCACCCGGCTTCGT

RXS02587 - 3'-Region
 TAAAAAGGCCTACACCGTCATGG

RXS02590 - 5'-Region
 GCCCCAAAGGCTTAAAGTAATGGGCATGCCCACTCCTTCTTCGACCAAAAGCTACGCTGCGGTCTTACC
 TCCACCTGGCCCCCTCGTGGGCTGGTTCCCTC

RXS02590 - coding Region
 ATGGGCATCTCATTGTTGTCATCACTGTTGAAAATCCATGGTTTTCCAGTCGTCGCAGATTTCTTCTTC
 GCGTTAGCTGTTGTGGTGGCAATTGTCATTATTGGCGGTTGGCTAATCTACCGCTCTCCTTCATTCAAA
 ACTGAAGTCATGCCGGCATGGGCAATGCTGTCCATGGGTTTGATCGCATGGGAACTGCAAGCCCCGTA
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 CCTCTTGTCACGCCGATGGTTGCTTCCACCTCGGCAGCACAACTCCATGAGCACTTTGAACCTCCGGCG
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 TATTCTACTATTTTCGGCCCCAAGGCGCAGGGCATCCCCTGATGGCAACACCAACATCATGGATTCCCT
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 ATCACAATGGGCATTATTTACGGCATCATCATGGGAATTTTACGATTCCCTTGGGAGCCATCGCTCAC
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 GTTGGCACTTTGAGTTTGGGTGCGCATTTTTTATCACAGAGCACCGGAGTGGAGTGGTTTAACTACTTC
 AGCCTGTACTTGATTGCTTTAATGCTCTTTCATGTCATCGTGTCCACCATCGCCGGTACGATTGCAGTA
 ATGAGAAGAATCGTCGGAAAGCTTAAATCTCAACTGGCC

RXS02590 - 3'-Region
 TAAATTGCAGCGAGAGGTCTAAA

RXS02932 - 5'-Region
 CACTACTGCGTTAAGGTATGAAAGTTCGCACACCAGCGATTTAATTCTGTGCCCACTAGCACGACC
 ATTTAGTTTTAACTTTCTTGGAGTTTCTA

RXS02932 - coding Region
 GTGTCCAAAACAGAAGAAGGCCGTTTCAGCGGCCATAATTATTTACGCGTTTCCAACCTTTCATTCTGCTG
 GCGCGATCATTTGCGTTTATCTTCCCGGAACCATTCATTCCGCTGACAACTACATTAATATCTTCCTC
 ACGATCATCATGTTTACCATGGGTTTGACCTTGACGGTGCCGATTTTCAGATGGTGCTTAAACGTCCA
 CTGCCTATCTTGATCGGTGTAGTCGAGTTTGTTCATCATGCCATTCCCTGGCGATCGTGGTTGCGAAA
 ATGTTCAACCTCAACCCAGCACTCGCCGTTGGCCTTCTCATGCTGGGATCCGTTCCGGGTGGCACCTCC
 TCCAATGTGATTGCGTTTCTCGCCCGAGGAGATGTCGCGCTATCGGTCACCATGACCTCTGTGTCCACC

CTCTCGCAACTCTTCGTGCAGATGCTGAGACCTTCGCTGATGACACCGGCGCGACGTATGGCATTACTG
GCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGGCGACGTCTTGGTTCCTTACGTTT

RXS03124 - 3'-Region
TGATCGTTTTGGTTCTAGCGTTC

RXS03125 - 5'-Region
TGACACCGGCGCGACGTATGGCATTACTGGCGTCACCCCAATTTACGATGACATCTCTGCTCGCCTCGG
CGACGTCTTGGTTCCTTACGTTCTGATCGTT

RXS03125 - coding Region
TTGGTTCTAGCGTTCCTCGTGTGCTGTTCCGGTCCATTTGGGTCCCATTTGATCGCGGCTCTG
GGCTTTGGCTTGTGAGTTCTGGCTACCTTTGGTGCTACCGTGCGGATCTTCCAAGAAGGTGCTTTCGGC
ATCATCGACGATCCTCAGCCACTGCTGTGCTTC

RXS03220 - coding Region
ATGGGCTTAAGGGAAATTTTGTCCAGCAAGTGGCTTGTGCGCATCCTCCTGGTAGGTATCGGATTGGGT
GTCGCACAGCAGCTGACCGGCATCAACTCCATCATGTACTACGGCCAGGTTGTTCTCATTTAGGCTGGT
TTCTCCGAGAATGCAGCTCTGATCGCCAACGTGGCGCCAGGAGTGATCGCAGTTGTCCGGTGCATTTCATC
GCACTGTGGATGATGGATGGTATCAACCGCCGTACCACCCCTCATTACCGGTTATTCTCTCACCACCATT
AGCCACGTATTGATCGGTATCGCATCCGTAGCATTCCAGTCGGCGATCCTCTTCGCCCCACGTTATC
TTGACTCTGGTTGTGGTCTTCGTGGGATCCATGCAGACCTTCCTCAACGTAGCTACCTGGGTTATGCTC
TCTGAGCTCTTCCCGCTGGCAATGCGCGGTTTCGCAATCGGTATCTCAGTGTTCTTCTCTGGATCGCA
AACGCGTTCCTCGGATTGTTCTTCCCAACCATCATGGAAGCAGTAGGACTAACCAGAACCTTCTTCATG
TTCGCGGAATCGGTGTGGTTCCTTGATCTTACATCTACACCCAGGTTCTTCAAACCTCGTGGACGTACC
TTGGAGGAGATTGATGAGGATGTTACTTCCGGTGTCATTTTCAACAAGGACATCCGAAAAGGAAAGGTG
CAC

RXS03220 - 3'-Region
TAAAAACCCAGACACTGCATAGATAACACG

RXS03221 - 5'-Region
CAAAAGTATTCAAAAAAGTTTGTATGTACGATTGACGGGACATATCGTGTCTGCCACGATTAAAGAC
ATTGGTGATGTGAATCACTGCCTACTACATC

RXS03221 - coding Region
GTGTTTCGTGACCCTGCACCTCCAAGTAAGGGCACGACAACTTAGGAGACAAGATGGCTAGTACCTTC
ATTAGGCGGACAGCCCTGAAAAAAGTAAGAAGCTGCCCCACTCACAGAAGGTCCGTATAGAAAGCGG
CTATTCTACGTTGCACTAGTTGCGACGTTTGGTGGGCTGCTCTTCGGATATGACACCGGAGTAATCAAC
GGTGCACCTCAACCAATGACACGTGAGCTCGGACTAACCGCGTTTACCGAGGGTGTTGTAACCTTCTTCC
CTGCTGTTTGGTGCAGCAGCTGGTGCAGATGTTTTTCGGTTCGATTTCCGACAACCTGGGGTCGCCGAAA
ACAATCATCTCACTTGCAGTAGCTTTCTTTGTCGGCACCATGATCTGCGTGTTGCTCCATCTTTTGCA
GTAATGGTTGTGCGACGTGTGCTTCTTGGACTCGCAGTTGGTGGCGCTTCCACTGTTGTCCCTGTCTAC
CTGGCTGAACCTTGTCTCTTTTGAAATCCGTGGCTCACTGGCTGGCCGTAATGAGTTGATGATTGTTGTT
GGTCAGCTCGCAGCTTTTGTCTCAATGCGATTATTGGAAATGTTTTTGGACACCACGATGGTGTGTGG
CGCTACATGCTGGCAATTGCCGCAATCCAGCAATTGCCCTCTTCTTTGGAATG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00001 (1-1128, translated) 376 residues
MATVTFK DAS LSYPGAKEPT VKKFNLEIAD GEFLVLVGPS GCGKSTTLRM LAGLENVTDG
AIFIGDKDVT HVAPRDRDIA MVFQNYALYP HMTVGENMGF ALKIAGKSQD EINKRVDEAA
ATLGLTEFLE RPKKALSGGQ RQRVAMGRAI VRNPQVFLMD EPLSNLDAKL RVQTRTQIAA
LQRKLGVTTV YVTHDQTEAL TMGDRIAVLK DGYLQQVGAP RELYDRPANV FVAGFIGSPA
MNLGTFESVKD GDATSGHARI KLSPETLAAM TPEDNGRITI GFRPEALEII PEGESTDLSI
PIKLDFVEEL GSDFSFLYGKL VEGDGLGSSS EDVPESGQIV VRAAPNAAPA PGSVFHARIV
EGGQHNFSAS TGKRLP

> RXA00002 (1-684, translated) 228 residues
VLHREGKGGL LGAYIAGFEW GLEKDYHVLC EMDADGSHAP EQLHLLLEEI EKGADLVIGS
RYVPGGETVN WPANRELLSR LGNKYISVAL GAGINDMTAG YRAFRRELLE HLDFEELSNA
GYIFQVDVAF RAIKDGFDVR EVPITFTERE LGESKLDGSF VKDSLLEVTK WGVHRSEQI
SDFTSEVSKI ASRTVKDMEL GPKATTAKNA VPDFVSEVSN LAKGTFFK

> RXA00089 (1-999, translated) 333 residues
MATPASAPTS EPRLKRTRAK LFDWKLLIGI IFVAGLVVLS LLTGQYDIFG GDDGQLMFEA
VRIPRTVSLI LSGAAMAMCG LVMQLLTQNK FVEPSTTGTT EWAGLGLLFV IYFVPAATVL
DRMLGAVVFS FIGTMVFFLF LRRVTLRSSL IVPIIGIMLG AVVSSISSFF ALQFDMLOQL
GTWFAGSFNT VFRGQYEV LW IVVIVVIAVF FFADRLTVAG LGEEIATNVG LNYNRMVLIG
TGLIAIATGV VTVVVGSLPF LGLIVPNVVS MFRGDDLRSN LPWVCLTGIA IVTICDLISR
TIIAPFEIPV SVILGIIGAV VFVIMIVRQR GRG

> RXA00090 (1-1119, translated) 373 residues
VAVDKDIENR TSDLSRWETM EESATVEGRT DVELASAPSK RRTSGAFQTA RAKRRYWIIM
AALLVTALAF TWGLIWKYKNP MPVGHPAFAL IAERRMESVF VMLIVAVCQG FATVAFQTVT
NNRIITPSIM GFESLYTLIH TSTVFFFGAT ALLATRNLEM FVGQLVIMVL LTLVLYTWLL
SGKRGMHAM LLVGIIIGGG LGSISTFMQR ILTPSEFDIL SARLEGSVNN AETEFPIAV
PLVVVASVLL LLSSRRNLNV GLGKDAATNL GINHRRSSII TLVLVSVLMA VSTALVGPMT
FLGLFVATLA YQFADTYDHR YILPMSALIG FVVLSGAYFV MNHVFRAGQV VSIIEMVGG
TVFLIVILRK GRL

> RXA00099 (1-1173, translated) 391 residues
VKNPRLIALA AIILTSFNLR TAITALAPLV SEIRDDLGV S ASLIGVLGMI PTAMFADAAAF
ALPSLKRKFT TSQLLMFAML LTAAGQIIRV AGPASLLMVG TVFAMFAIGV TNVLLPIAVR
EYFPRHVGGM STTYLVSFQI VQALAPTAV PISQWATHVG LTGWRVSLGS WALLGLVAAI
SWIPLLSLQG ARVVAAPSKV SLPVWKSSVG VGLGLMFGFT SFATYILMGF MPQMVGDPQL
GAVLLGWWSI LGLPLNILGP WLVTFTNCF PMVVIASVMF LIGNGGFCLA PDVAPWLWAT
LSGLGPLAFP MALTILNIRA ETSAGASALS SFGQGLGYTI ACFGPLLTFG IVDATGSFRT
IFLLFAGATL FVIRGGYFAT RQVYVEKLLN R

> RXA00123 (1-1119, translated) 373 residues
MPKNYDINGA IRRRDMLRRR YLPDSANSTP VP EEVSPITR YVTDGIPKRP PLGATVADGL
KFAEGASNRM VMSLYPAPSK PAIEELAEAW DLHPTIVEDL LLGQQRPKLD RYEDIIFIAI
RSARYIDSRE EVDFSEFHIL MKPQAIILC QDNQWIDGTS AASFNP EEI DKRIKTL LAD
AELLSSGPRA AAYRL LDAIV DGFSPVLRGI AIDQEQIERQ VFSGDAVAE RIYNLSQEII
DMQHTTSSVT EVVQRLNKDF IRSGMSEELR AYLDDVADHL TRDNTRVSEY RESLSQILNV
NATLVAQRQN EDMKKISGWA AIIFAPTLVS SIYGMNFDIM PELHWAFGYP LALLAMLGFT
LLLYWIFKRS KWM

> RXA00160 (1-573, translated) 191 residues
MLNIARNRNM KRRLAIAAFV ATATATATMA PASAQTDYAG LSSGVADTVA EAAGVATTAV
APAATVARPA NGTFTSGFGP RWGTFHNGID IANSIGTPIY AVMAGTVISS GPASGYQWI
RIQHDDGSIS IYGHMEYLYV SVGERVAAGQ EIAGMGSQGF STGSHLHFEI HPDGVTPVDP
QAWLANHGIY V

> RXA00193 (1-843, translated) 281 residues
MQATLKKYFP VFVLP TLLAF MIAFLVPPFIV GFFLSFTKFT TITNAKWVG I DNYVKAFSQR
EGFISAFGFT VLVVIVSVIT VNIFAFLLAW LLTRKLRGTN FFRTVFFMPN LIGGIVLGYT

WQTMINAVLS HYATTISADW KFGYAGLIML LNWQLIGYMM IIYIAGLQNV PPELIEAAEL
 DGVNKEWMLR HVTIPMVMPs ITICLFLTLS NSFKLFDQNL ALTNGAPGGQ TEMVALNIIN
 TLFNRMNVEG VGQAKAVIFV VVVVVIAYFQ LRATRSKEIE A

> RXA00203 (1-912, translated) 304 residues
 MLNNGALVGL IALCVGLFIA TPHFLTIPNL INIGIQSATV AILAFGMTFV IVTAGIDLSV
 GSVAALGAMT SAYFFAEVGL PGWITLLIGL FIGLLAGAIS GISIAYGKLP AFIATLAMMS
 IARGITLVIS QGSPIPSAPA VNALGRTYFG IPMPILMMAL AGIVCWFILS RTVLGRSMYA
 IGGNMEAARL SGLPVKKILV MVALAGVYA ALAGLVMTGR LSSAQPPQAGV GYELDAIAAV
 VIGGASLAGG TGKATGTLLG AILLAVIRNG LNILNVSSFW QQIVIGCVIA LAVGFDVIRN
 KTSK

> RXA00204 (1-1572, translated) 524 residues
 MVNSEQALHQ HDPAPILQLD KVSKEFGPVN VINQVSDVDR PGRVLALLGE NGAGKSTLIK
 MMSGVYQPDG GQILVDGKPT TLPDTKTAEs FGIATIHQEL NLVPTMTVAE NVMLGRTPRK
 WGLVNFKHLR RQAQAALDLI GVDVDLNAQV GSLGIARQQM VETAKALSMN ARILILDEPT
 AALTGREIDQ LFKVVDQLKE KGVAMVFISH HLDEIARIGD TVSVLRDQGF IAELPADTDE
 DELVRLMVGR SIENQYPRSA PEIGQPLLEV KNLNAEGRFT DISLTVRAGE VVGLAGLVGA
 GRTEVVRSIA GVDKVDSEGE IVAGKKLRGG DISEAIKNGI GHIPEDRKAQ GLVLGSSVED
 NLGLATLAST ARAGLVDRSG QHKRAAEVAE KLRIRMASLK QPISDLSGGN QQKAVFGRWV
 LAGSNVLLLD EPTRGVDVGA KVEIYNIINE MTEKGGAVLM VSSELPEVLG MADRILVMSG
 GRIAGELPAK GTTQDDVMAL AVSQVDDSiT EEAIAEIENT KEDR

> RXA00270 (1-888, translated) 296 residues
 MIGAFEFGLL YGVVALGVYL TFRVLNFPDL TVDGSLLTGA ATAATALMSG WPPLMATAAG
 FVTGFIAGMI TGLLHTKGKI DGLLAGILTM IALWSVNLRI MGGANVPLLR TDNLFTPLRD
 AGLLGTWAGP AILAVAVGIL GLIVIWFLNT DIGLSLRSTG DNGPMVQSFC VSTDFTKILT
 ISLSNGFVGL AGALIAQYQG FADISMGIGL IVIGLASVIL GQAIFGQRRV WLAVLAVIVG
 AIAAYRLIIFA ALRVGLDPND MKAISAILVV VAMLLPRWRA KFSKAPKPKQ PVAVEA

> RXA00311 (1-855, translated) 285 residues
 MEHSPEGKRK FFTSSVMAGC SVGNVLAGLV FIPFLMLPEE HLMSWGWRVP FLISALVIVV
 AYFVTRILEE ASTEKAEDA GAPALAVLRT QGIDVARVEL ITFFAVVQTT FNVYALAYAA
 NEIGIDRSFM VMVNTIALGL SIGTIPLAAW VSDRIGRKPV LLFGAITCAI TTYFYFQAIS
 EADLVLFAL CLVNQGLFYS CWNGVWTIFF PEMFASSVRY TGMAMGNQLG LIIVGFAPTI
 ATALYAWNGW EAVAGFIIGA IALSAAVILT TKETAFTKLE DLGKK

> RXA00312 (1-426, translated) 142 residues
 METVRTATAA PETASLKLRE AESPAKSPKK AALASLLGST LEYYDFVIYG TASALLFNHL
 FFPQGDVVA TIGSLASFGV AYIARPIGGL VMGHVGDKIS RKTALMVTLM IMGIASISIG
 LLPTYGQIGI WATVLLMIAR IA

> RXA00345 (1-951, translated) 317 residues
 MAGMKKLLWT LPILPLVLAG CSTGSADSAD STNAAGSNSL KVVSTSTQVWA DVAEAVAPDV
 DIEAIIITGGD IDPHSFEPsA TDMAKVSEAD IIVGGGGYD SWLYGTLEDD DRIIHALDLS
 EHDHSEHDDH EHEAEEAHEH DHDEEGHDHD VDNEHVWYST EYVSEVAEEF AEKVTELDPE
 AQADATAVTT KMDELHNQIH DLPVRIAQT EPIADHILSH SDMVESTPEG YRATTLESE
 PTAADVASFQ DAINNGDLV LIYNPQSAST VATSLKDLAE EKGIPVVEIY ETPQNTENFL
 DAFKAVDDL TAATNQV

> RXA00378 (1-1773, translated) 591 residues
 KSWRSYPSWF AFDHGTLTQN EIYFDVACGI TVLLLAGRLL TRRRSQSSLL AELGRLQIDP
 QRIVTVVRKH RLKRVVQELN IPVQEVVRND DVKVPNTTI PVDGTVIGGG SRIAASIIMG
 QDQRDVKVND KVFAGSLNLE SEIKVRVIRT GHRTRIAAVH RWVKEATLKE NRHNRAAIRS
 AGNLVPITFT LAVVDFCLWA LISGNINAAF TTTLAVLACV APVALALSAP LATRNSIEAA
 ARHGILVRSG EIFRVLDDVD TAVFNRVGTI TDGEMTVETV TADKGEDPEL VLRVAGALAM
 ESHHAISKAL VKASREARDT GAGGEDVPHW IEVGNVEITE AGSFQATIEL PLIKPSGEKI
 MRTTEALLWR PRSMTEVREH LSPRLVAAAT SGGAPLIVRW KGKDRGVITL SDHVRSDSSD
 AIIAIEEQGI ETMMLSRDty PVARRYADSL GITHVLGIA PGKKAQVVRA VHTRGSTVAM
 IGDESVMDCI KQADVGVLMG VDRPSDLRDD SDDPAADVIV MREEVMSVPT LFKLARRYAK
 LVNGNIALAW IYNGVAMVLA VSGLLHPMAA TVAMLASSLL IEWRSGRARK Y

> RXA00412 (1-1080, translated) 360 residues
 VSHTASTPTP EEYSAQQPST QGTRVEFRGI TKVFSNNKSA KTTALDENVTL TVEPGEVIGI
 IGYSGAGKST LVRLINGLDS PTSGSLLNG TDIVGMPEK LRKLRNIGM IFQQFNLFQS
 RTAAGNVEYP LEVAKMDKAA RKARVQEMLE FVGLGDKGKN YPEQLSGGQK QRVGIARALA
 TNPTLLLADE ATSALDPETT HEVLELLRKV NRELGITIVV ITHEMEVVRV IADKVAVMES
 GKVVVEYGSVY EVFSNPQTQV AQKFVATALR NTPDQVESED LLSHEGRLFT IDLTETSGFF
 AATARAAEQG AFDNIVHGGV TTLQRQSFQK MTVRLTGNTA AIEEFYQTLT KTTTIKEITR

> RXA00413 (1-897, translated) 299 residues
 MKLRRITTTA IAGLFAATAL VACGSDSDGS STTVAEGTEG VTIRIGTTDA AKEAWTVFED
 KAAEEGITLD IVPFSDYSTP NEALAQDQLD VNLFOHLKFL AEYNVGSAGD LTPVGSSEIV
 PLALFWKDDH SIDGIDGESV AIPNDPSNQG RAINVLVQAG LVTLKTPGLV TPAPVDIDEA
 ASKVSVIPVD AAQAPTAYQE GRPAIINNSF LDRAGIDPNL AVFEDDPESE EAEPYINVFV
 TKAEDKDDAN IARLVELWHD PEVLAAVDRD SEGTSVPVDR PGADLQEILD RLEADQENA

> RXA00431 (1-675, translated) 225 residues
 MVSIDTYNAC VDFPIFDAKS RSMKKAFLGA AGGAIGRNQD NVVVVEALKN VNLHLREGDR
 VGLVGHNGAG KSTLLRLLSG IYEPTRGSAD IRGRVAPVFD LGVGMPEIS GYENIIIRGL
 FLGQTRKQMK AKMEEIADFT ELGEYLSMPL RTYSTGMRIR LALGVVTSIE PEILLDEGI
 GAVDAAFMAK ARDRLQALVE RSGILVFAST QRLSCQLCNT ALWVD

> RXA00444 (1-777, translated) 259 residues
 LLIPATLAML LIIGPIFALL LQIPWDRSWE LLTAPESLGT ARLSIGTALF STALCAIVGF
 PLALALHLYE RSHPRVTSVL TVLVYAPLVL SPVVSGLALT FLWGRRGFLG SWLDQVGLPI
 AFTTTAVVEA QVEVALPFFI STVTTALRGI PKQFEEIAAT EGATRWEIMH KMI I PLAMPG
 IFTGMILGFA RALGEYGATL TFAGNIAGVT RTIPLHIELG LSSNDMDKAL GAVIMLLAVY
 VLIIGAIGAL RLESKVRKV

> RXA00445 (1-912, translated) 304 residues
 MADLSIEHVS RFFGDAIALN DVSLTVPSGS ITAIIGPSGS GKTLLRLLA GLDSPDEGTV
 SIGNKIAKLG DTALCFQDSP LYPHLNVWEN VAFPLKLKAT NTADDEVVKKR VSDVLEMLEI
 APLARRKITE LSGGQKQVRG IARALVRDVE VYLFDEPMAH LDQALARDIV ADLRKIQQSL
 GLTFVYVTHS KSEAFALADQ IVVLVDGQVA QVGEAEELVE KPKTLEIAEF LSPTELVRR
 RGDAVEAWRP EDTQLARGGT ATVEAVTYLG REWLVTQTEG HAVSEEKFDV GESVTLTQKK
 VFSF

> RXA00466 (1-987, translated) 329 residues
 VQSRLSKILR SSVVGVAULA LLAGCSNNAD DTDADSTSTG NSAFPVSIEH EFGTTTIDDV
 PERVVTLGVT DADIVLALGT VPGNTGYKF FENGLGPWTD ELVEGKELTL LDSDSTPDLE
 QVAALEPDLI IGVSAGFDDV VYEQLSDIAP VVARPAGTAA YAVAREEATN LVARAMGQSE
 KGQELNEETD ALIQAARDEN PSFDGKTGTV ILPYQGYGA YLPGDARGQF LDSLGISLPE
 AVLSRDTGDS FFVDVPAESV KDVDGDVLLV LSNDENLDIT AENPLFETLN VVQKDAVIVA
 TTEERGAITY NSVLSVPFAL EHLAPRIAE

> RXA00482 (1-648, translated) 216 residues
 MRISKLVTI ALLAAISLFG ISTAQADIF DGRLAGGSS QVSNLSSVPE NLALPEIENS
 IDLERYKQKW YQVAAIPQPF SLQCSHDVTA DYGVDSDTI SVTNKCGTFF GPSVIEGSAK
 VVSNASLKVS FPGIPFQSED NQANYRVTYI EDDYSLAIVG SPSRSSGFIL SRTPQLSSDQ
 WSHVRNITED SGWWPCAFIT VPATGGLNTA TPLCTL

> RXA00523 (1-750, translated) 250 residues
 VLRNQLASPD IIGISSGASA AGVICIVFFG MSQSAVSAIS LCASLAVALL IYLVAYRGGF
 SATRLILTGI GIAAMLNSLV SYLSKADSW DLPTATRWLT GSLNGATWDR AMPLIVTTVV
 LIPLLVANAR NVDLMRLGND SAVGLGVATN RTRVIAIIAA VALIAVATAA CGPIAFVAFV
 SGPIAARILG SGGSLIIPSA LIGGLIVLIA DLIGQYFLGT RYPVGVVTGA FGAPFLIYLL
 IRSNRAGVTL

> RXA00525 (1-660, translated) 220 residues
 MSLAESILLA LTSLRSNKMR ALLTLLGVII GIASVIGILT IGKALQDQTL NSLES LGAND
 LSAQVEERPD EDSPEPDMFA FSGAANSSGN LIPEETVDTL RDRFAGSITG ISVGGMGTOG

TLIGDTADLK SDLLGVNEDY MWMNGVEMNY GRAITQDDVA AQRPVAVIAP DTFNTLFDAN
PNLALGSEVA FELNGQETFL RVIGVYKEAA AGGLVGSNPT

> RXA00556 (1-594, translated) 198 residues
YTPYTVANDI THTKDGLNTL SIRAAQGVDDQ DSLKGSLLQTY FDALYANNDS HHVAMLDLFRK
QIEEFNTILG AMSLGISAIG GISLLVGGIG VMNIMLVSVT ERTREIGVRK ALGARRRDIR
LQFVVEAMII CFIGGILGVL LGGILGLIMS SAIGYISLPP LSGIVIALVF SMAIGLFFGY
YPANKAAKLD PIDALRYE

> RXA00596 (1-453, translated) 151 residues
MLNALKFIPW LIGQIFLSGF SVITAAVKKD TGFNPVVIRY PLRVTTDFQI AALSTCITAT
PSTLSLGLRE PRKPGDPTIL LIQAVFGSDP VEVFESIADM EQRLVPSVAS IDHGVPGQGP
YKEIRPSDAE WPSREIADTA QNTVSQDKRE F

> RXA00634 (1-1383, translated) 461 residues
MWERFSFYGM QALLVYYLYF DVAAGGLGLD QTQATGLVGV YGALLYLCCW AGGWVSDRVL
GAECTLLGGA ISVTIGHLVL AGLGGKIGLA IGLGCIAGS GFVKTAATV LGSRHGEQEG
DAKADPAFQL FYLGINVGAL LGPLLTGWLS SRYSEFMGFG AAIVLMIGGL GIYAALRKPM
LQSFPLEVKK ALLRAQNPAE KHVISTAFAA VAVLCGVLLY LLLTETVSAD QLAGALLLV
IGAALWLIIQ PLRHPQVSSE EKRKVLAFIG IFVCSTAFWA VQAQTYGVLA VYSQERVDRM
VGDFEIPAAW SOSLNPFIL ALSIPISLWF MRGSRAPRVK IGISIGVIA GSGLLVLIPIF
VGMPLAPVWV LPLSVFLISL GELFIGPGGM AATAHHAPRI FATRESALYF LTLAIGMSIA
GNVSKFYDPT NHTSELRYFA VFGISIIIVG VGSMLVAKKV G

> RXA00665 (1-438, translated) 146 residues
MSSSTLLLAS GQVTALAADY TLSHTPSDGI LVLVGFAMIL TFMTLIMLGR LTPMVAMLLV
PTIFGLIAGA GLGLGDMALD AIKDMAPTAA LLMFAIMFFG IMIDVGLFDP LIRVITRVLH
DDPAKVIGT AVLAGVVS LD GDGSTT

> RXA00702 (1-1320, translated) 440 residues
LGLPPAVMRK RVEETLDBLLG IAEIRYVPLA ELSGGEQQRV AIGAVLTTRP ALIILDEPTS
ALDPNGAEDV LATVTKLAHD LAMTVVLAEH RIERVLQYVD RVAHVAGADGH VTVGTPEEIM
ADSDVAPPIV ELGRWAGWAP LPLSIRDARA HSADMRKRLY QRGVLVKNLH NHAVQPLLIA
EDIMVDFPEI RAVDGVNLNL NSGEITVLMG RNGCGKSSLL WALQSGGTRN QGSVQVLDEA
AGFSWTDPKT LKPAKRRNLV SMVPQTPTDI LYESTVHAEL ARSDKDAAAP AGTTREILDS
LVPNIPDHLH PRDLSEGQKL SLALSIQLAA KPRVVFDEP TRGLDYDGKK SLARSFQQLA
DDGHAILVVT HDVEFSALCA DRVLFMASGK IISDGTAVEI LPASPAYAPQ VAKITAGIQE
ESHWLTVSAV KAALGHGEIS

> RXA00728 (1-792, translated) 264 residues
VAAAIIVALL AWFIIISALNN EAYGWDITYRS YLFDTRIATA ALHTIALTLL SMILGVVLGA
ILAVMRMSGN PVMQGVAWLY LWIFRGTPYI VQLVFWGLLG SLYQSINLGF AEIDLQSLLS
NMFLLAIVIGL GLNEAAYMAE IVRSGIQAVP EGQMEASKAL GMNWSMTMRR TILPQAMRII
IPPTGNELIS MLKTTSLVVA IPYSLELYGR SMDIAYSLFE PVPMLLVAAS WYLVITSILM
VGQYYLEKHF EKGSTRTLTA RQLA

> RXA00732 (1-822, translated) 274 residues
MLVQMTSTLM ISAPMLAIGG IIMAVRQDLG LSWMVVSIP VLIIVVALII VRMVPLFQTM
QKRIDRINQI IREQLTGIRV IRAFVREDVE RERFTTASKD VADIGVRTGN LMALMFPAVM
LIMNLSAVAV IWFGAFQVES GETQIGTLFA FLQYIMQILM GVMMAAFMFV MVPRAAVSAD
RIGEVLETP SVQAPETPAQ PSTSAGEIVF NNATFAYPGA DDPVLNNVSF RVAPGSTTAI
IGSTGSGKTT LIGLVPRLFD VTEGDVTVDG TDVR

> RXA00734 (1-453, translated) 151 residues
RHLRYGNEDA TETQLWQALA IAQAADFVRE MPEGLDSEIA QGGTNVSGGQ RQRLAIARAL
LKQPEIYIFD DSFSALDVST DAALRRALST NLPDATKLIV AQRVSTIRDA DQIVVLNNGE
VVGIGTHTNL LNTCGTYREI VESQETAQAQ S

> RXA00759 (1-924, translated) 308 residues
MLRYVGRLL QMIPVFFGAT LLIYALVFLM PGDPVQALGG DRGLTEAAAE KIRQEYNLDK
PFIVQYLLYI KGIFVLDFGT TFSGQPVIV MARAFPVTIK LAIMALLFES ILGIIFGVIA

GIRRGGIFDS TVLVLSLIVI AVPTFVIGFV LQFLXGVKKG LLPVTVGSNT SITALIMPAV
VLGAVSFAYV LRLTRQSVSE NLRADYVRTA RAKGMSGFNV MNRHVLRLNSL IPVATFLGAD
LGALMGGAIV TEGIFGINGV GGTLYQAILK GEPTTVVSIV TVLVIVYIIA NLLVDLIYAV
LDPRIRYA

> RXA00760 (1-1032, translated) 344 residues
MPNNEFHTNH SLGQDDQTPD QAHFFPQGRG EALVRPGQEH FIAATDETGL GAVDAVADDS
APTSMWGEAW RDLRRRPLFW VSAVLIILAL LLAAVPQLFT STDPQFCVLA NSLDGPQSGH
PFGFDRQCD IFARTVYGAR ASVAVGVLT LVALIGTVF GALAGEFGGI MDTILSRITD
MFFAIPVLVA AIVVMQMFKE HRTIVTVVLV LGLFGWTNIA RITRGAVMTA KNEEYVTSAR
ALGASKAKIL LSHIMPNAAL PIIVYATVAL GTFIVAEATL SFLGIGLPPS IVSWGADIAG
AQTSLRTQPM VLFYPAMALA LTVLSFIMMG DVVRDALDPK SRKR

> RXA00761 (1-591, translated) 197 residues
MTTNIPQTPN HEGEQPLLEL KDLKISFTSS TGVVDAVRGA NLTIYPGQSV AIVGESGSGK
STTAMSIIGL LPGTGKVTEG SIMFDGQDIT GLSNKQMEKY RGSEIGLVPQ DPMTNLNPFVW
RIGTQVKESL RANHVVPGE MDKRVAEVLA EAGLPDAERR AKQYPHEFSG GMRHRLALIAI
GLAARPKLLI ADEPTSA

> RXA00774 (1-654, translated) 218 residues
MDKATDALLR TSLASAESAL GNAEKLEELR TGCESQAVEL LALETPVARD LRQVVSIIYI
VEEITRMGAL AMHVANSVRR RYPDPVIPED MRGYFKEMAR LAADMTDHIR QILIDPEPDL
ALEMAKSDDA VDDLHQHIMR ILTLRPWPHD TKSVDLTLL SRFYERYADH TVNVAARIYI
LSTGLHPEEY MEKREQQRAD ADMEKRWAEL ERQFRTSE

> RXA00775 (1-771, translated) 257 residues
MSKLKINDVN IYYGDFHAVQ NVNLEVPARS VTAFIGPSGC GKSTVLRISIN RMHEVTPGAY
VKGEILLDGE NIYGSKIDPV AVRNTIGMVF QKANPFPTMS IEDNVVAGLK LSGEKNKKKL
KEVAEKSLRG ANLWEEVKDR LDKPGGGLSG GQQQRLCIAR AIAVEPEILL MDEPCSLDP
ISTLAVEDLI HELKEEFTIV IVTHNMQQAA RVSDQTAFYS LEATGRPGRL VEIGPTKKIF
ENPDQKETED YISGRFG

> RXA00776 (1-921, translated) 307 residues
MTNNVVTPRM DEPLKKSSAF TDISSSRKTT NTAATVIIYG AMLIAAVPLV WVLWTVISRG
IAPILTADWW STSQAGVMLM LPGGGAHAM IGTFMQAVVT SVISIPIGIF TAIYLVEYSN
GNRLGRLTTF MVDILTGVPS IVAALFVYSL WIVLFGFDRS GFAVSLSLVI LMVPVIIRNT
EEMLRVVPQD LREASYALGV PKWKTIKIV LPTALSGIVT GVMLAVARVM GESAPVLVLV
GSSQAINWNP FGGPQASLPL MMLDMYKAGT APATLDKLGW AALTIVLIIA VLNIGARIIS
AKFSVKQ

> RXA00777 (1-1065, translated) 355 residues
MATNESVSEK QRLDTRVQA HPVAVNANSS QTKPSKKIVA EGGGSVKRPG DRIFEVLSTA
SAAIITAIII AIAAFLIWRV VPALMRNAEG IGGFFTYSGA WNTTDIDAMY FGIPNLLAAT
LLISVIALII AMPIALGIAI FLSNYSKRL VKPLGYMVDL LAAVPSIVYG LWGWQVLGPA
LSGFYTWIES WGSFFLFAT YQNSPSFATG RNMLTGIVL AVMLPVEIA TAREVFIQTP
KGHIESALAL GATRWEVVRL TVLPFGMSGY VSGAMLGLGR ALGETMALYM VVSPSSAFRE
SLFDGGTTFA TAIANAAPF NDNTRACAYI SAGLVLFALT FIVNAGARAM VNRGK

> RXA00828 (1-369, translated) 123 residues
EHQFVARTVR DELEIGPKIM KVDASERIEE LLDRLRLRHL ENANPFTLSG GEKRRLSVAT
ALVAAPKLLI LDEPTFGQDP ETFTELVTML RELTDNGISI VSVTHDPDFI AALGDHHIEV
SAK

> RXA00832 (1-555, translated) 185 residues
TLTAVVYGGF LFRQMGAAQAG EFQEVEVAEK ADDAAKWEVP FRGLILIIITV LPIVLLSHDM
ATVMDEVLAS LGAPVAMAGL IIATIVFLPE TITSLKAAWT GEIQRVSNLA HGAQVSTVGL
TIPAVLVIGV ITGQDVVLGE TPINLLLLGT TIAVTIAIFS SKKVS AVHGS VLLMLFGVYM
MSMFA

> RXA00934 (1-789, translated) 263 residues
PSFSMAALPF AEGPIVATYH ASSSGSKLLK AFLPVLSPML EKVRAGIAVS EMARRWQVEQ

VGGDPVLIPN GVETSMFKAA RQIEPNPVE IVFLGRIDES RKGLDILLRA LTRLDRPFTC
TVIGGGTPRE VAGINFVGRV SDEEKAAILG RADIYVAPNT GGESFGIVLV EAMAAGCAVV
ASDLEAFSLV TDSEAAQPAG VLFKTGSDAD LAKKLQALID DPSSRSTLIA AGLKRANAYD
WSTVSTQVMA VYETIAIDKV RLG

> RXA00939 (1-168, translated) 56 residues
GVLLGGVTMS IGLMVHEASV LLVIAIAMLL LRPTLKEDKD KADVSTADAA KETLSA

> RXA00942 (1-204, translated) 68 residues
LSTKNYHVEG LTCANGVASV EDEIGIVAGT QGVDIDIETG RVTVTGEGFT DEEIIIEAVAN
AGYKVSGR

> RXA00950 (1-906, translated) 302 residues
MNTPAVQVQN LSLSFGSFTA VNGLSLTVEQ GSIHGFLGPN GAGKSTTIRA LIGVLKPQTG
SVAILGQDPV AHPDVLRRVG YVPGDATLWD NLTGAEVFRA LESLRKTPSN RALENELIDA
FQLDPSKKIR EYSTGNRRKV SLIAALSHEP ELLIVDEPTA GLDPIMEQVF VTYVRKARTN
GASVLLSSHI LSEVEQLCDY VTVLKEGRAV ASNEVSYLRK ISAHRITATI PAVPQHLAGR
GEVDFDAGHL SITCDASEVP DILRIIIDAG QQDIISTAAS LEEIFLRHYG ETVSGSESKA
SQ

> RXA00960 (1-459, translated) 153 residues
LKNDVDVNVA GFVVPLCATI HLAGSMMKIG LFTFAVVMY DMEVGVGLSI GFLMLGITM
IAAPGVPGGA IMAATGMLAS MLGFNTEQVA LMIAAYIAID SFGTAANVTG DGAIIVIVNK
FAKGQLHTTS PDEIEEDDRV AFDITPSDVE HHK

> RXA00980 (1-639, translated) 213 residues
MFVGVNGHAI GIVAVADAVR SDSASAIESL HKAGIQVMA TGDHRVAQN VASKLGVDEV
YSELLPEQKL ELVRDLQAAG KTVAMVGDV NDTPALAAAD IGVAMGVAGS PAAIETADIA
LMADRLPRLA HAVTLAKRTV RTMRINILIA LATVMVLLAG VLFGGVTMSV GMLVHEASVL
LVISIAMLLL RPTLKEDAAQ ASDIKRSEIQ QIA

> RXA01000 (1-540, translated) 180 residues
MLAARGVGPY WLRTVLRVFE AVIRAFPEVV IAIILLTVTG LTPFTGALAL GISGIGQQAQ
WTYEAIESTP TGPSEAVRAA GGTTPEVLRW ALWPQVAPSI ASFALYRFEI NIRTSAVLGI
VGAGGIGSML ANYTNYRQWD TVGMLLIVVV VATMIVDLIS GTIRRRIMKG ASDRVVAPSN

> RXA01002 (1-417, translated) 139 residues
PTEHDKQIAF HALESVGILD KVVTRAGALS GGQKQVAIA RALSQDPSVM LADEPVASLD
PPTAHSVMRD LENINNVEGL TVLVNLHLID LARQYTTRLV GLRAGKLVYD GPISATDKD
FEAIYGRPIQ AKDLLGDRA

> RXA01003 (1-804, translated) 268 residues
MTTPSSTLIP QKPRAGVKTY LIIGAIVVFT VATATPALGG IELDFASIAA NWRNGANKLL
QMLQPNFAFL PRTWLPMLET LQMALVGAVL SAAVSVPLTL WAAQATNTSA IGRGIVRTII
NVVRSVPDLV YATILVAMVG VGALPGILT FLFNLGIVVK LVSEAIDSTE HPYMEAGRAA
GGSQFQINRV SALPEVMPLF ANQWLYTLEL NVRISAILGI VGAGGIGRLL DERRAFYAYA
DVSVIILEIL IVVIVIEVIS NALRKRLV

> RXA01006 (1-858, translated) 286 residues
MTTSQILRRI GQAVLVLLVT FTLAFIMLSA LPGDAVSARY SSPDLGLSPE QIAQIRESYG
ADESLIAQYF STLGGFLVGN FGYSVQTGTA VATQLAEALP GTLTALILAF LLAAILALVI
SILATMDRFA WIKGIFQALP PFFVSLPSFW LGIILIQIVS FRLGWVPVIG TTPAQGLILP
TITLSIPITA PLAQVLIRSI EEVKAQPFIA AVRARGAGEM WIFFRNIIRN ALLPTLTIAI
ILFGELVGGA VVTEAVFGRA GLGQMTVNAV ANRDMPVMLA IVVIAA

> RXA01012 (1-1641, translated) 547 residues
MTTPLLEIND LVVSYQTAKG LVHAVNNVSL EVHPGQITAI VGESGSGKST TAQAVIGLLA
DNAEVDSGRI SFNGRSLVGL NAREWKNVRG TKIGLIPQDP NNSLNPVKTI GASVGEGLAI
HKRGTAERK KKVIELLERV GIDNPEVRYD QYPHELSSGM KQRALIAAAI ALEPELIAD
EPTSALDVTV QKIILDLED MQRELGMGIL FITHDLAVAG DRADRIVVMQ KGEVRESGYA
ASVLTDPQHE YSKLLADAP SLTIGEIPTR VPAVDPEVAQ AKGPLLVVDK FRKEHQKGKE

GAFVAANDIS FEVLPGTTHA IVGESGSGKT TLGRAIAMFN TPTSGSISVS GKDITNLSKA
 QQRELQQIQ LVYQNPYSSL DPRQTIGSTI AEPLRNFTKV SKQEADEKVA HYLELVALDP
 ALATRRPREL SGGQRQRVAI ARAMILEPEL VVFDEAVSAL DVTVQAQILR LDDLQRELQ
 LTYVFISHDL AVVREISDTV SVMSRGNQVE LGKTAEVFNN PQTDFTRRLI DAIPGSRYRG
 GELNLGL

> RXA01013 (1-795, translated) 265 residues
 LGNPWTRPAA VISIVVLAVA VLMALVPGLF TSQDPFTGDD VALLGPSGTH WFGTDSVGRD
 LYSRVYGAR ETLLGALIAV LVGLIVGTIL GLLAGAQRGW VDTVLMRFVD VLLSIPALLL
 SLTVIILLGF GTMNAAIAVG ITS VATFARL ARSQVMTVAG SDFVEAAAYGS GGTQAQVLF
 HILPNSLTPV FALAALQFGS AILQLSVLGF LGYGAPAPT EWWGLLISDAR DYMATSWWLT
 VLPGFVIIAV VMSANYLSRI IQKEA

> RXA01070 (1-1386, translated) 462 residues
 MANATAQKGR FGLPGWMTGF GAQVIAGLIL GLILGLVARG MDSGAADGEA SWLTGLLSGV
 GSAYVSLKV MVPPLVFAAV VTSVAKLREV ANAARLAVST LVWFAITAFF LSVGLIAVAL
 IMQPGVGSTV DASNAADPSR VGSWLGFQIS VIPSNILGLS GSYSENSGVN LSFNVIQILV
 ISIAIGVAAL KAGKSAEPFL KFTESFLKII QIVLWWIIRL APIGSAALIG NAVATYGWSA
 LGSGLKFVLA IYVGLAIVMF VIYPVVLKLN GIPVLGFFKR VWPVTSLGTV TRSSMGVMPV
 TQRVTEQSLG VPSAYASFAI PLGATSKMDG CAAVYPAVAA IFVAQFYGID LSIMDYVLIM
 IVSVLGSAAAT AGTTGATVML TLTSLTLGLP LAGVGLLLAI EPIIDMGRTA TNVTGQALVP
 AIVAKREGIL DQDVWDAAEK GGAAIEMATV SEKETEPAEV RS

> RXA01094 (1-948, translated) 316 residues
 MTLATIPSP QGVWYLGPIR IRAYAMCIIA GIIIVAIWLTR KRYAARGGNP EIVLDAAIVA
 VPAGIIGGRI YHVITDNQKY FCDTCNPVDA FKITNGGLGI WGAVIDLGLA VAVFFRYKKL
 PLAPFADAVA PAVILAQGIG RLGWNFNQEL YGAETTVPAW LEIYYRVDEN GKFAVPTGTS
 TGEVMATVHP TFLYELLWNL LIFALLMWAD KRFKLEHGRV FALYVAGYTL GRFWIEQMRV
 DEATLIGGIR INTIVSAVVF AGAIIVFFLL KKGRETPEEV DPTFAASVAA DAVASPRKRP
 LPKAGEGIDG ETPSTR

> RXA01135 (1-324, translated) 108 residues
 VTHILFDSRR FLQLGAFASL STALAGAARY VTSTSNNEPA DNTPLTIGYV PIAGSAPIAI
 ADALGLFKKH GVNVTLLKYS GWSDLWTAYA TEQLDVAHML SPMTVAIN

> RXA01141 (1-462, translated) 154 residues
 VNSAADLKG MVLGIPFEYSV HALLLRDYLV SNAVDPIADL ELRLLRPADM VAQLTVEGID
 GFIGPGPFNE RAISNGSGRI WLLTKQLWDK HPCCAVAMAK EWKAEHPTAA QGVNLAALEEA
 SAILSNPAQF DSSARTLSQE KYLNQPATLL DGPS

> RXA01142 (1-420, translated) 140 residues
 TRTHLEQVGL TDAAERRPAR LSGGMQQRVG IARAFADIPP IMLLDEPFGA LDALTRRELQ
 LQLLNIWEAS RRTVVMVTHD VDEAILLSDR VLVMSKSPEA TIITDIPVNL PRPRHELSED
 ASVEAETAL RKRMLHLEH

> RXA01164 (1-1575, translated) 525 residues
 VTLFVRLALA AVGGFLVFAS NEPIGWFWAG IVGTALFFIS LAPWDLGVPQ KRRKKNEPVP
 FLQQMSTGPT VVQGMLLGFV HGLVTYLQLL PWIGEFVGS PYVALSVVEA LYSIALGAFG
 VLIARWRDWK VLLFPAMYVA VEYLRSSWPF DGFVAVRLAW GQINGPLANL AALGGVAFVT
 FSTVLAAGV AMVIISKRL AGAIIASVI AIGAVSSLYV DRNGTSDESI EVAAIQGNVP
 RMGLDFNAQR RAVLANHARE TLKLDEQVDL VIWPENSSDV NPFSDAQARA IIDGAVEHVQ
 APILVGTITV DEVGPRNTMQ VFDPVEGAEE YHNKKFLQPF GEYMPFREFL RIFSPYVDSA
 GNFQPGDGTG VVEMNAANLG RAVTVGVMT C YEVIFDRAGR DAIANGAEFL TTPTNNATFG
 FTDMTYQQLA MSRMRAIEFD RAVVVAATSG VSAIVNPDGS ISQNTRIFEA ATLTESIPLK
 DVTITAAARVG FYVELLLVII GVLGLFAIR MNSRSKSAKG SARPA

> RXA01168 (1-720, translated) 240 residues
 RTATPDVHVL IVDDNSPDGT GERADKLAAD DDHIFVLHRE GKGGCLCAEYM AGFQWGLERD
 YQVLCMDAD GSHAPEQLHL LLAEITNGAD LVIGSRYVPG GRVVNWPKNR WLLSKGGNVY
 ISVALGAGLT DMTAGYRAFR REVLEALPLD ELSNAGYIFQ VEIAYRAVEA GFDVREVPIT
 FTEREIGESK LDGSFVKDSL LEVTKWGLKH RGGQAKELSK EMVGLLLNYEW KHFKKRNTWL

> RXA01185 (1-858, translated) 286 residues
 MTDPEPNSQGT PQICPTDPTT QALAVRGLTK SYGDATVVNN INLDIPKGAI YGIVGPNAG
 KTTMLSMATG LLRPNKGTAW ISGFNVWEPP NDAKRSMGLL ADGLPIFDRL TGKELLTYVG
 ALRELDGEGIV DQRSEELLEA LGLKEAAGKR VVDYSAGMTK KILLAQALIH NPKVLILDEP
 LEAVDPVSGR LIQQILKNFA QTGGTVVLS HVMELVEGLC DHVAIINRGV VEIAGHVNEV
 RRGSRYSRMSS LMRLKALLFK RGHYLGWVRP KAIKAKAKIRT RIGLSK

> RXA01188 (1-1104, translated) 368 residues
 MMNGVVQPQE HLDATLIAAD FHGNPENS GD RKERLNFQGW KYALNRTVRD VFPDGLLDLA
 ALLTFFSILS IAPAVLLGYS VITIFLASDS TEILNLVRDE VNQYVPEDQS HVVNGVIDSI
 AGSAAAGQVG VAVGVITALW TSSAYVRAFS RCANAVYGRS EGRTLIKRW A MLLFLNLALL
 LGIILVSW VLNETLVMGI FAPIAEPLHL TNVLSFLTDR FMPIWIWVRF PVIVGVLMIF
 VATLYYWAPN ARPWKFRWLS LGSFLAIVGI LLAGVGLNFY FTLFAAFSSY GAVGSLLAVF
 IALWVFNICL IIGLKIDVEI SRAKQLQAGM PAEDYSLVPP RSIEKVAKM K QRQQLMDQA
 AAIREESN

> RXA01245 (1-1767, translated) 589 residues
 ASWVTTLGLG GFHLDFFWEL ALLVTIMLLG HWLEMRALGA ASSALDALAA LLPDEAEKV
 DGTTRTVAIS ELAVDDVVLV RAGARVPADG TIMDGAAEFD EAMITGESRP VYRDTGETTV
 AGTVATDNTV RIRVEATGGD TALAGIQRMV ADAQASSRA QALADRAAAL LFWFALITAL
 ITAVVVTIIG SPDDAVVRVAV TVLIIACPHA LGLAIPLVIA ISSERAAKSG VLIKDRMALE
 HMTIDVVLV DKTGTLTGEGA HAVTGVPAT GIAEGELLAL AAAAEADSEH PVARAIVTAA
 AAHPEASQORQ LRATGFTAAS GRGIRATVDG AEILVGGPNM LREFNLTPG ELADITGSWA
 QRGAGVLHV V RDGEIIGAVA VEDKIRPESR AAVRALQARG VKVAMITGDA TQVAQAVGKD
 LGIDEVFAEV LPQDKDTKVT QLQERGLSVA MVGDGVNDAP ALARA EVGIA IGAGTDVAME
 SAGVVLASDD PRAVLSMIEL SHASYRKMVQ NLVWATGYNI VAVPLAAGVL APIGVLLPPA
 AAAILMSLST IIVALNAQLL RRIDLDPAHL APTDGKEEKA AVSSAAPVR

> RXA01247 (1-234, translated) 78 residues
 VAAATDATPE GPTYQVTGM TCGHCADNVT EAVSALPQVD DVQVDLIAGG VSIVTVTGSV
 PLETVHRAIE ETGYTVLS

> RXA01285 (1-543, translated) 181 residues
 PQTSIAPEGI RYVDLIARGR APYQSLIQW RTSDEDAVAQ ALASTNLTEL AARLVDELSG
 GQRQRVWVAM LLAQQTPIML LDEPTTFLDI AHQYELLELL RAFNEAGKTV VTVLHDLNQA
 ARYADHLIVM KDGHVHATGT PEEVLTAEMV QGVFGLPCII SPDPVTGTPT VVPLSRSRAG
 A

> RXA01289 (1-1044, translated) 348 residues
 MTAVAVEKQK ETSISKNLGR RRALGILGIV VALGALIVLS IAVGANPLSF SSVWQGFTHA
 DSSEASIIWV SMRIPRTL VG IVTGAAFGVA GALIQALTRN PLADPGILGV NAGAGFAVTV
 GVGFFGLSSV TGYIWFALG AAAATLLVYF IGASTSGSVN PVALVLAGVA LAAVLGGVTS
 FLTLIDPETF ESIRNWNLGS VARTDLSDTM TVLPFLAVGL ATALLLSGAL NSIALGDDLA
 ASLGTKVMRT RVLGIISVTL LAGGATALTG GIGFVGLMVP HVVRWVVGPD QRWIITFSAL
 CAPVLVLGAD ILGRIIARPG EIEVGIVTAV IGAPVLIALV RRRKASGL

> RXA01290 (1-1164, translated) 388 residues
 VVFNISRTD ETPVAASEPV ESTRPVSEAS TSPALNPGYH AVSVQRRRFS FRIPARLMV
 SLILFAIALC SATWAITMGD YPLSLGQVIN ALAGTGEKFQ LLVVREWRLP VAIAAVVFGA
 LLGIGGAIFQ SITRNPLGSP DVIGFDAGSY TAVVLVILVL GNTHYWSIAF AAIVGGIVTA
 FAVYVLAWRK GVQGFRLLIV GIGVSAMLSS VNAYLITRAD VEDAMVVGFW SAGSINRITW
 QSLLPSLVIA AVIIVAAIVL ARSLRFMEMG DDVATTLGVK TNSTRALIV VGVATSALVT
 AAAGPISFIA LVAPQLARRL TKTPGVSLVA AAAMGSALLS CAHLLSLIIS SFYRTIPVGL
 LTVSIGGCYM IWLLLRETRR QYRTGTIR

> RXA01297 (1-798, translated) 266 residues
 MGYVGMVLAI LFIGLPLVFI VLTSFKQQSE IYTPVTFWP SEFNFDNYAN VFERVPFLNY
 FRNSIIITVI LCLVKIILGV ISAYALSILR FPGRNLVFL VISALMVPSE VTVISNYALV
 SQLGWRDTYQ GIIVPLAGIA FGTFLMRNHF MSIPSELIEA ARMDHCGHER LLWKVLLPIS
 MPTLVAFSMI TVVNEWNQYL WPFLMAETDN SATLPIGLTM LQNNEGVSNW GPVMAATIMT

MLPVLVMFLA LQEYMIKGLI SGA VKG

> RXA01298 (1-393, translated) 131 residues
FVWKNLGYSF VIYLAALQGL NKDLSEAAPV DGASAWTRFW KVTLPQLRPT TFFLSITVTL
NSVQVFDIIH TMTRGGPLGN GTTTLVYQVY TETFTNYRAG YGATIATILF LLLLIITVIO
VRYMDKENKQ K

> RXA01303 (1-1335, translated) 445 residues
VTQLNTKGVV LQGWDPEDPE HWDSKIAWRT LWITTFSMII GFCVWYLVSA IAPLLNRIGF
DLSAGQLYWL ASIPGLAGGL IRLIYMFLPP ILGTRKLVGI SSGFLFLIPMF GWFLAVQDSS
TPYWLLTLA ALTGIGGGVF SGYMPSTGYF FPKAKSGTAL GIQAGIGNLG VSIIQFMGPW
VMGFGLLGIG FLTPQRTIEG TTVFVHNAAI VLVPWTILAA VLSFLFLKDV PVTANFRQQI
DIFGNKNTWI LSIIYLMTEG AFAGFAAQFG LIINNNEGIA SPMAETYPAE MLHAGATFAF
LGPLIGALVR AAWGPLCDRF GGAIWTFVGG IGMTIATAAA AIFLSRAETP DDFWPFLWSM
LALFFFTGLG NAGTFKQMPM ILPKRQAGGV IGWTGAIGAF GPFIVGVLLS FTPTVAFFWG
CVVFFIIATA LTWIIYARP N APFPG

> RXA01323 (1-2265, translated) 755 residues
MAQTPAKIPA ALNFIDVDLG VTGMTCTSCS ARVERKLNKL DGVEATVNYA TESAQVSYDP
SKVSPEQLIK TVEDTGYGAF TMASAAAEE EDNAPADSGQ SRIDAARDHE AADLKHRVIV
SALLSVPVVL VSMIPALQFN NWQWAVLTLV TPIFFWGGSP FHKATWANLK RGSFTMNTLV
SLGTSAADLW SLWALFIENA GHPGMKMEMH LLPSASTMDE IYLETVAVVI TFLLLGRWFE
TKAKQSSEA LRKLLDMGAK DAVVLRDGAE VRVPVNQLKL GDVFITRPGE KIATDGEVDE
GSSAVDESML TGESIPVEVT KGSKVTGATL NTSGRLMVKV TRIGADTTLS QMAKLVTDAQ
SKKAPVQRLV DQISQVFVPV VIVIAIATLI AHLVFTDAGL APAFTA AVAV LIIACPCALG
LATPTALLVG TGRGAQLGLL IKGPEILEST KKVD TIVL DK TGTVTGTMS VTDVTAINYS
ETEILEFAAA VESASEHPIA QAIKAAAEHE QVTDFQNTAG QEVTVGVVRGH EVRVGRPSST
LIDALLHPFQ HAQKIGGTPV VVTIDGVDSG IITVRD TVKD TSAE AIRGLK ELGLTPILLT
GDNEGAAKSV AA EVGIDQVI ANVLPHEKVQ NVEALQAQ GK NVAMVGDGVN DAAALQAQDL
GLAMGAGTDV AIEASDITLM NNDLRS AVDA IRLSRKTLGT IKGNLFWAFA YNVALIPVAA
IGLLNPMLAG IAMA FSSVFV VSNSLR LRGF KARSN

> RXA01338 (1-1878, translated) 626 residues
MLFIRSF DGI ITVAALVAIA IHLILWLALD LDGLAKNWPL IAIVIVGGIP LMWDVLKSAI
KTRGGADTLA AVSIITSVLL GEWLVA AIIIV LMLSGGEALE EAASRRASGT LDALARRAPS
TAHRLLGATI LDGTEEI AVE EITVGDLVAV LPHELCPVDG EIVAGHGTMD ESYLTGEPYV
VSKSKGSQAM SGAVNGDTPL TIVATKLAHD SRYAQIVGVL HEAENNRPEM RRMADRLGAW
YTVIALALGG LGWIVSGDPV RFLAVVVVAT PCPLLI AVPV AIIG AISLAA RRGII VKNPG
MLENASGVKT VMFDKTGTLT YGRPVIDIH TAPGVEEDTV LALAASVERY SRHPLADAIR
EGAKARELHL PDVVEVSERP GQGLTGT VGE HLVRITNRRS TLEIDPDSKN YIPVTSSGME
SVVLVDDKYA ALIRLRDEPR ASASEFIAHL PKKHKVDKLM IISGDRASEV RYLADKVGID
EVHAEASPED KLNIVNRHNE HGATMFLGDG INDAPAMAVA TVGVAMGADS DVTSEADAV
ILDSSLERLD DLLHISARMR RIALQSAGGG MALSVIGMIL AVFGFLTPLM GAIFQEVIDV
LAILNSARVA LPRGAISDFD TQEKVS

> RXA01395 (1-1086, translated) 362 residues
MAVMAYQPAD NRYDDMIYRR VGNSGLKLPA ISLGLWHNFG DDKPLSTQRS IIHRAFD RGV
THFDLANNYG PPAGSAETNF GRILREDLKS HRDELISSK AGWDMWPGPY GFGGSRKYL V
SSLDQSLTRL GLDYVDIFYH HRPDPDTPLE ETMYALRDIV ASGKALYVGI SSGPELTAE
AAEFMAEEGC PLLIHQPSYS IINRWVEEPG DDGENLLQSA ANNGLGVIAF SPLAQGLLTD
KYLDGIPEGS RASQGSXXX XXLNVNIDX VXXXXXXXXX TGQSFXKXKF CWVVAQPRKV
RRRITVTSAL IGASSVEQLD NSLDSLNNLE FSDAELEAID EISHDAGINI WAKATDSKTR
EN

> RXA01411 (1-327, translated) 109 residues
FIAQVMLGIG AVTANCVTSV MMAEVFQEV T RGTSAGITYN VTYAIFGGSA PFISTALVSW
TGSPLAPAVY MIIIALFAFT ASRFIPETSP VEV TATPAIK APKVLVNPG

> RXA01454 (1-267, translated) 89 residues
MMLIVAFLIA LVGHYLMGGI RAGNQMTGQK SFVSRGARTQ LAVTAGLWML VKVAGYWLD R
YDLLTKENST FTGASYTDIN AQLPAKIIL

> RXA01455 (1-462, translated) 154 residues
 VTWIFAIIL VILIAPMSVG FYTDWLWFGF VDFRGVFSKV IVTRIVLFEVI FALIAGFVTW
 LAGYFVTKLR PDEMSAFDTQ SPVYQYRQMI ENSLRRVMVI IPIFVALLAG LIGQRSWRTV
 QMWLNGQDFG VSDQQFGLDY GFYAFDLPLM RLIA

> RXA01625 (1-201, translated) 67 residues
 MAIKNYTVEG MTCGHCVSSV KEEVGEVAGV TAVDVTLETG AVQVTGEDFT DEAVKAAVVE
 AGYKVVA

> RXA01756 (1-1308, translated) 436 residues
 MKELELGEAR DVAATLEAMP IQEVIDQVER TSITKGAVLL RLLSKDRSLL VFDALGPRLO
 ADLIGAFQDA EVLDYFADLD PDDRVSLLE LPASIADELL RSLDPQEKQV TELVLGYAKG
 SVGRWMSPOV LLLFDDMSVA EVLDFVRNHA AEAETIYALP IVNRARQVMG VVSLRKLFA
 DPTLKVSEIM VRPVSVLASA DIEETARWFL QLDLVAMPVV DESNMLLGVL TFDDAQDIVE
 QADSEDSARS GGSEPLQPY LSTPIRKLKVK SRIVWLLVLA VSAILTVQVL DIFEATLVEA
 VVLALFIPLL TGTGGNTGNQ AATTVTRALA LGDVRKSDVF RVLGREIRVG LMLGALLGAV
 GFVIASLVYG MPVGTVIGLT LLAVCTMAAS VGGVMPIIAK AIGADPAVFS NPFISTFCDA
 TGLIIYFAIA KLVVGI

> RXA01808 (1-1119, translated) 373 residues
 MRGGAPARTS KPGFRLEAAE ALIAEVPAPR DKVELMAFSK SRQGRVVIEL EDATVATPDD
 RILVEDLTWR LAPGERIGLV GVNGSGKTTL LRTLAGEQPL QAGKRIEGQT VKLGWLRQEL
 DDLDSLRLI DCVEDVASV MMGDKQVSAS QLAERLGFSP KRQRTPVGDL SGGERRRLQL
 TRVLMAEPNV LLLDEPTNDL DIDTLQELLES LLDGWPGTMV VISHDRYLIE RVTDSWALF
 GDGKLTNLPQ GIEEYLQRRR AMAAAEDSGV INLGAATQAG TFSAAEQAA TSVESGSISS
 QERHRITKEM NALERKMGKL DQQMDKLNQQ LADAAEAMDT IKLTELDTKL RAVQEEHGE
 EMQWLELGE IEG

> RXA01822 (1-582, translated) 194 residues
 MARQNSNTGG LRLVLVGIGT GAFLGAARDF FMVRADITGA STVQLWSAGS LSGRDWNHAL
 LVLISCAVIV PALCIIVRRL RLMEMGDDAA GALGISVERT RLIAILLAVL LVGIATAAAG
 PIAFIALAAP QIARALARED GVLVAASISI GSGLLVAADC LEQHVDTELH TPVGLVTSLL
 GGVYLMWLLS RKEA

> RXA01890 (1-720, translated) 240 residues
 MASIVFENV T RKYSPGARPA VDKLNLEIAD GEFLVLVGPS GCGKSTSLRM LAGLEPIDEG
 RLLIDGKDAT ELRPQDRDIA MVFQSYALYP NMTVRDNMGF ALKNQKVAKA EIEKRVAEAS
 RILQLDPYLD RKPAALSGGQ RQRVAMGRAI VREPSVFCMD EPLSNLDAKL RVSTRAEISG
 LQRRMGVTTV YVTHDQVEAM TMGDRVAVLL LGVLQQVDTP QNLYDYDPAVA FVASFIGSLP

> RXA01900 (1-1299, translated) 433 residues
 MTTAVDQNSP PKQQLNKRVL LGSLSGSVIE WFDFLVYGTV AALVFNKMYF PSGNEFLSTI
 LAYASFSLTF FFRPIGGVIF AHIGDRIGRK KTLFITLMLM GGGTVAIGLL PDYNAIGIWA
 PILLMFLRIL QGIGIGGEWG GALLLAYEYA PKKQRGLYGA VPQMGISLGM LLAAGVISLL
 TLMPEQFLT WGWRIPFVGS ILLVFIGLFI RNGLDETPEF KRIRDSGQQV KMPLKEVLTK
 YWPAVLVSIG AKAAETGPFY IFGTIYIYAYA TNFLNIRDNI VLLAVACAAL VATIWMPLFG
 SFSDRVNRV LYRICASATI VLIVPYLVL NTGEIWFALFI TTVIGFGILW GSVNAILGT
 IAENFAPEVR YTGATLGYQV GAALFGGTAP IIAAWLFEIS GGQWWPIAVY VAACCLLSVI
 ASFFIQRVAH QEN

> RXA01939 (1-603, translated) 201 residues
 STSGTDLTSL SHKEIFQMRR KLQVVFQNPY GSLDPMYSIY RCIEEPLTIH KVGGRKARE
 ARVVELDMV SMPRSTMRRY PNELSGGQRO RIAIARALAL NPEVIVLDEA VSALDVLVQN
 QILTLLAELQ QELKLTLYLFI THDLAVVRQT ADDVVVMQKG RIVEKGRDDE IFNDPQQHYT
 RDLINAVPGL GIELGTGENL V

> RXA01972 (1-594, translated) 198 residues
 VATGLLSAIG LFIATNIDDI IVLSLFFARG AGQKGTTLRI LAGQYLGFMG ILAAAVLVTL
 GAGAFPLPAE IPYFGLIPLA LGLWAAWQAW RSDDDDDDDA EIAGKKVGVL TVAGVTFANG
 GDNIGVYVPV FLNVDTAAVI IYCIVFLVLV AGLVLLAKFV ATRPPIAEVL ERWEHVLFP

VLIGLGIFIL VSGGAFGL

> RXA01986 (1-618, translated) 206 residues
 MASTFIQADS PEKSKKLPL TEGPYRKRLF YVALVATFGG LLFGYDTGVI NGALNPMTRE
 LGLTAFTEGV VTSSLLFGAA AGAMFFGRIS DNWGRRTII SLAVAFFVGT MICVFAPSFA
 VMVVGRLVG LAVGGASTVV PVYLAELAPF EIRGSLAGRN ELMIVVGQLA AFVINAIIGN
 VFGHHDGVWR YMLAIAAIPA IALFFG

> RXA01995 (1-654, translated) 218 residues
 MDIRQTINDT AMSRYQWFIV FIAVLLNALD GFDVLAMSFT ANAVTEEFGL SGSQLGVLSS
 SALFGMTAGS LLFGPIGDRF GRKNALMIAL LFNVVGLVLS ATAQSAGQLG VWRLITGIGI
 GGILACITVV ISEFSNNKNR GMAMSIYAAG YGIGASLGGF GAAQLIPTFG WRSVFAAGAI
 ATGIATITATF FFLPESVDWL STRRPAGARD KINYIARR

> RXA02033 (1-789, translated) 263 residues
 MPLSGKIGGF IVAVVFLAA LSFIWTFDFP VQAFPQERLE GSSLRHLLGT DRYGRDVLSQ
 IMVGSRVTLV VGIIAIAIAA LIGTPLGIAA GMRRGMVETF VMRGADLMLA FPALLLAIIS
 GAVFGASTWS AMVAIGIAGI PSFARVARAG TLQVTSQDFI AAARLSKVSS ARIALRHILP
 NITSMLIVQA SVAFALAILA EAALSFLGLG TTPPDPSWGR MLQTAQASIG VTPMLAVWPG
 AAIALTVLGF NLFGDGLRDA IDP

> RXA02034 (1-966, translated) 322 residues
 VSKTIAWTVL RYTLTFVIAS IIIFVLIRVI PGDPAVALG ITATPEAIAA LQSQLGTDQP
 LFQQYFSWIG GMLTGDFGTS LSSGQDLSP IFDRLQVSLI LVGCSIVLSL LIAIPLGVLS
 ARRGVVISG ISQIGIAIPS FLAGILLVAV FAVGLGWLPA NGWIPPSNF GGFLARLILP
 VLALTAVQAA ILTRYVRSV MDVMGQDFMR TARSKGMSFN RALIIHGLRN AALPVLTVTG
 LQLTTLVIGA VVIEQVEVIP GIGSMLESV SNRDIAVQS IVMLLVAFITL LVNLVVDLLY
 QVVDFRVGAV GVASTKVP GS VA

> RXA02035 (1-1509, translated) 503 residues
 MKITRGLLPS LLLASTIVVS SCSAGSTAYQ QPPAVDQSSI VIATTAAAS LDFTNAAGAA
 IPQAMMSNIY EGLVRIDAEG EIQPLLATSW DISDDRTEYI FHLREGVLFS NGDPFNADSA
 KFSIDRVKTD WTNGLKSGMD VVESTVIDD HTLVSLVRP SNQWLWSMGT AIGAMTEGG
 VDKLATDPVG TGPYTVTHWA PGRAIGFGAR ADYWGQKPLN DAATIRYFSD ATASTNALQS
 GDVDVIWAMQ APEQLATLQE YTVEVGTTNG EMLLSMNNQR APFDDVRVRQ AVMEFIDRQA
 VIDTALEGYG TDTGGVPVPP TDPWYEKSTM YPYDPDRARA LLEEAGAEGT RITMSIPSLP
 YAQAASEILY SQLRDVGFDV VIESTEFPV WLAQVMGQKD YDMSLIAHVE PRDIPTLFSP
 NYLGFDDTE TQALLAEADS SANEVELMQQ AVDRIMEQAV ADNLNMVANI VVMSPEITGI
 DPNVVSAGLE LSLIGRKESG VAQ

> RXA02062 (1-1170, translated) 390 residues
 MRVGMMTREY PPEVYGGAGV HVTETLRFMR EIAEVDVHCM GAPRDMEGVF VHGVDPALES
 ANPAIKTLST GLRMAEANN VDVVHSHTWY AGLGGHAAAR LHGIPHVATA HSLEPDRPWK
 REQLGGGYDV SSWSEKNAME YADAVIAVSA RMKDSILAAY PRIEPDNVRV VLNGIDTELW
 QPRPTFDDAE DSVLRSLGVD PQRPIVAFVG RITRQKGVEH LIKAAALFDE SVQLVLCAGA
 PDTPEIAART TALVEELQAK REGIFWVQDM LGKDKIQEIL TAADTFVCP S IYEPLGIVNL
 EAMACNTAVV ASDVGGIPEV VVDGTTGALV HYDENDVETF ERDIAEAVNK MVADRETAAK
 FGLAGRERAI NDFSWATIAQ QTIDVYKSLM

> RXA02068 (1-1119, translated) 373 residues
 IFVPMRLRIA IEPKDITLVT GSVSLRTRFV RTGELQVMGD IVGAKVHTDD PELQQFHGRA
 VEIADVELEL SRTRDWIITR VAVLGERPKF GRRPVLHTVP WSHIHGITAG GVGESNHTAE
 LIAGFEDMRP ADVAKQLYQL PTAQRTEVTE ELDDEKLADI LQELSEDROA ELIEELDIER
 AADILEEMDP DDAADLLGEL PDDKADVLLD LMDPEESAPV RRLMDFSPDT VGALMTPEPL
 IMPDSTTVAE ALAMARNPDL PTSLASLIFV VRPPTATPTG KYLGCVHLQK LLREPPSSLI
 GGILDPDLPP LYADDSQETA ARFFATYNLV CGPVLNENRH LLGAVAVDDL LDHMLPEDWR
 DAGIRPGKEH THG

> RXA02079 (1-615, translated) 205 residues
 MSEAFDATKV RKAULTVALL NFAYFFVEFF IALSAGSVSL LADSVDFLED TSINLLIFIA
 LGWPLARRAV MGKLMIAVIL APAFAFAWAA IQRFSAQAP EVFPIIVASL GAVVINGASA

IIISRVQRHG GSLGQAAFLS ARNDVLINIA IIMMALITAW TTSGWPDIL L GCFIILLALH
AAHEVWEVSE EERLASKALA GEAD

> RXA02096 (1-1317, translated) 439 residues
MGLDVSDEQI EHAARLAQAH DFIDRLPNKY EEVIGERGLT LSGGQRQRIA LARAFLAHPK
VLVLDDATSA IDASTEDRIF QALREELHDV TILIIAHRHS TLELGDRVGL VEDGRVTALG
PLSEMRDHAR FSHLMALDFQ DSHDPEFTLD NGSLPSQEQL WPEVSTKQY KILAPAPGRG
RGMSMPATPE LLAQIEALPA ATEETRVDA G RLRTSTSGFK LLSLFKQVRW LVVAVIALLL
VGVAADLAFF TLMRAAIDNG VQAQSTSTLW WIAIAGSVVV LLSWAAAAIN TIITARTGER
LLYGLRLRSF VHLLRLSMSY FERTMSGRIM TRMTTIDIDL SSFLQSGLAQ TVVSVGTLLG
VVTMLAITDA QLALVALSV PIIIVLTLIF RRISSRLYTA SREQASQVNA VFHESIAGLR
TAQMHRMEDQ VFDNYAGEA

> RXA02119 (1-1641, translated) 547 residues
MTETLVVNGL AGGYGHRTLF NDVNLTVAAG DVVGVVGVNG AGKSTFLKIL AGVEKPLAGT
IALSPADAFV GYLPQEHRT SGETIAVYIA RRTGCQAATT AMDDTAEAFG ADPDNAALAD
AYAEALDRWM ASGAADLDER IPIVLADLGF ELPTSTLMEG LSGGQAARVG LAALLLSRFD
IVLLDEPTND LDLDGLEQLE NFVQGLRGV VLVSHDREFL SRCVTTVLEL DLHQNSHHVY
GGGYDSYLEE RAVLRQHARD QYEEFAEKKK DLVARARTQR EWSSHGVRNA IKRAPDNDKL
RKKAASSE KQAKVQRME SRIARLEVE EPRKEWKLOF SVGKASRSS VSTLNDASF
TQGDFTLGPV SIQVNAGDRI GITGPNAGK TLLRGLLGN QEPSTGTATM GTSVAGIEID
QARALLDPQL PLISAFKHFV PDLPISEVRT LLAKFGLNDN HVERDVEKLS PGERTRAGLA
LLQVRGVNVL VLDEPTNHL D LEAIEQLEQA LASYDGVLLL VTHDRRMLDA VQTNRRWHVE
AGEVREL

> RXA02220 (1-2676, translated) 892 residues
VSSPLPAAVT SKPAHALSSD EVLENLGVQD TGLTSAEATQ RLEANGPNEL PQTPPETVWQ
RLFRQVNDPM IYVLIAAAVL TAFLGHWTDT IVIGAVVIIN MMVGFIQEGK AADALASIRN
MLSPESAALR DGVEFKIDAA ELVVGDVVKL SAGDKVPADL RMLAATNLHI EESALTGEAE
AVVKGTDPEV ADAGIGDRTS MAFSGTLVLT GSGTGVTAT GAGTEIGHIT TMLADVDSVD
TPLTRSMKKF SSALAIVCVF LAILMLVVAG LVHHTPLEEL ILSAIGFAVA AIPEGLPAVI
AITLALGVQK MAARNAITRR LNSVETLGSV TTICTDKTGT LTRNEMTVRA IATGTSLYDV
SGAGYEPLGE IRLKDGEQVS KQDFPDLYAM ALVAANVND EIIYQEDGMWR LSGETPDGGI
RAFAMKTNAE ILTRTAEVPE DSAYKYMATL HTIDGANTML VKGAPDRLLD RSAQQRNGEP
LDRPYWEQLI EDLASQGLRV LAAAYKELPH STSTITPEDV DQGELTFLGL YGIMDPPREE
VIEAMKVVSQ AGVRVRMITG DHSSTARAI A REVGIRGQNV LTGAETIAT DEELQGLVDN
ADLFVRTSPE HKLRVVRLQ ANGEVASMTG DGVNDAPALK QADVGVAMGI KGTEATKDA
DIVLADDNFA TIAGAVEMGR TIYDNLKAV VFMLPTNGAQ GLVIFIAMLL GWELPITALQ
VLWINLITAI TSLALSFEF AEPGIMNRKP RNPKSGLIDA PSVLRIVYVS LLLGGATFWA
FLGARDAGID IDTARTIAVT TLAVSQVFYL LSSRYFEVSA LRKELFTTNP ISWLCIALML
ILQLAFVYLP FMQSTFDATA LTLRDWVMP L VFGVVVFAV ETEKFIRRLK AS

> RXA02222 (1-375, translated) 125 residues
LGRPPPGDVH TLLDDIGAE SEADKVPIEW QNALTADRY ANRQHMSQAR LYRQLTSDVG
EGFTTEAAQY AIENVNADWN ANALVKARNY QERQAMSVDR IYRQLTSEHG EGFTPEQAQY
AIDNL

> RXA02312 (1-1359, translated) 453 residues
LSNRHLQLIA IGGAIGTGLF MSGSKTISVA GPSVILVYAI IGFMFFVMR AMGELLANL
NYKSLRDAVS DILGPGAGFV TGWTYWFCWI ATGMADIVAI TGYTQYWWPE IPLWLPGVLT
IALLFALNLA AVRLFGEFMEF WFAIIKIVAI VSLIVVGLFM VVTAFESPNG TTAQFNNLIE
HGGFFPNGIT GFLAGFQIAI FAFVGIELAG TAAAETENPT KTLPRAINSI PIRIVVFYVL
ALAVIMMVTP WDQVRADNSP FVQMFALAGI PAAAGIINFV VITSAASSAN SGIFSTSRML
YGLSLEGAAP KRWSRLSKNL VPARGLTFSV ICLIPAVGLL YAGGTVIEAF TLITTVSSVL
FMVVWSYILV AYIVYRRNSP ELHKKSIFKM PGGVVMMAVV LVFFAAMLV LSLEPDTRAA
LIATPVWFII LGIGWLSIGG AKGAKHRSQI TSH

> RXA02313 (1-1221, translated) 407 residues
MRVAIVAESF LPNVNGVTNS VLRVLEHLKA NGHDALVIAP GARDFEEEIG HYLGFIVRV
PTVRVPLIDS LPIGVPLPSV TSVLREYNPD IHLASPFVL GGAAFAARQ LRIPAIAYQ
TDVAGFSQRY HLAPLATASW EWIKTVHNM C QRTLAPSSMS IDELRDHGIN DIFHWARGVD

SKRFHPGKRS VALRKSWDPS GAKKIVGFVG RLASEKGVVER LAGLSGRSDI QLVIVGDGPE
 AKYLQEMMPD AIFTGALGGE ELATTYASLD LFVHPGEFET FCQAIQEAQA SGVPTIGPRA
 GGPIDLINEG VNGLLLDVVD FKETLPAAAE WILDDSRHSE MCAAWEVGVK DKTWEALCTQ
 LLQHYADVIA LSQRIPLTFF GPSAEVAKLP LWVARALGVR TRISIEA

> RXA02344 (1-678, translated) 226 residues
 MLNRMKSARP KSVAPKSGQA LLTLGALGVV FGDIGTSPLY SLHTAFSMQH NKVEVTQENV
 YGIISMVLWT ITLIVTVKYV MLVTRADNQG QGGILALVAL LKNRGHWGKF VAVAGMLGAA
 LFYGDVVITP AISVLSATEG LTVISPSFER FILPVSLAVL IAIFAIQPLG TEKVGKAFGP
 IMLLWFVTLA GLGIPQIIGH PEILQSLSPH WALRLIVAEP FQAFVL

> RXA02348 (1-1134, translated) 378 residues
 PIRVAWFCVV MPALILTYLG QGALVINQPE AVRNPMFYLA PEGLRIPLVI LATIATVIAS
 QAVISGAYSL TKQAVNLKLL PRMVIRHTSR KEEGQIYMPL VNGLLFVSVM VVVLVFRSSE
 SLASAYGLAV TGTLVLVSVL YLIYVHTTWK KTALFIVLIG IPEVLLFASN TTKIHDGGWL
 PLLIAAVLIV VMRTWEWGS RVNQERAELE LPMDFLEKL DQPHNIGLRK VAEVAVFPHG
 TSDTVPLSLV RCVKDLKLLY REIVIVRIVQ EHVPHVPPEE RAEMEVLHHA PIRVVRVDLH
 LGYFDEQNLP EHLHAIDPTW DNATYFLSAL TLRSLRPGKI AGWRDRLYLS MERNQASRTE
 SFKLQPSKTI TVGTELHL

> RXA02353 (1-468, translated) 156 residues
 MALLILAGLQ MIPKETYEAA RVDGATAWQQ FTKITLPLVR PALMVAVLFR TLDALRMYDL
 PVIMISSSSN SPTAVISQLV VEDMRQNNFN SASALSTLIF LLIFFVAFIM IRFLGADVSG
 QRGIKKKKLG GTKDEKPTAK DAVVKADSAV KEAAKP

> RXA02354 (1-789, translated) 263 residues
 MTKRRTKGLIL NYAGVVFIIF WGLAPFYWMV ITALRDSKHT FDTTPWPTHV TLDNFRDALA
 TDKGNNFLAA IGNSLVISVT TTAIAVLVGV FTAYALARLE FPGKGIVTGI ILAASMFPGI
 ALVTPLFQLF GDLNWIGTYQ ALIIPNISFA LPLTIYTLVS FFRQLPWELE ESARVDGATR
 GQAFRMILLP LAAPALFTTA ILAFIATWNE FMLARQLSNT STEPVTVAIA RFTGPSSFEY
 PYASVMAAGA LVTIPLIIMV LIF

> RXA02394 (1-1311, translated) 437 residues
 MLSPAAVAAL ILVIGIVVLI IASVPVAIAI GLPSLFAAMA VLGPENAAQA VAQRMFTGTN
 SFTLLAIPFF VLAGLLMNSG GIATRLIDAA KVLVGRMPAS MANTNIAANG LFGAVSGAAV
 ASASAVGTVM TPKMKEEGYS RAYAAVNVA SAPAGMLIPP SNTFIVYSLV SSTSIAALFM
 AGVGPGLLWI LACVIVGTWL ARKENYKREQ IHPTFKQSLV VLWRALPSLL MIVIVVGGIL
 LGWFTPTESA AIAVVYCLVL GFYRTIKVG DLADILLKAT RTTSIVMLLI AVSAALSWVM
 AFAKIPQMIS DALLSVSDSK VVILLIMFI LLLIGTVMDP TPAIILFVPI FLPVVTELGV
 DPVHFGAMVV MNLSVGVITP PVGNVLFVGS QVAGLRVETV IRRLWPYLIA IIVALFVVVF
 VPQISIWLP TMGLMGG

> RXA02402 (1-744, translated) 248 residues
 VSKTEEGRSA AIIYAFPTF ILLGAIIFI FPEPFIPLTN YINIFLTIIM FTMGLTLTVP
 DFQMVLRPL PILIGVVAQF VIMPFLAIV AKMFNLNPAL AVGLLMLGSV PGGTSSNVIA
 FLARGDVALS VTMTSVSTIV SPIMTPFLML MLAGTETAVD GGGMAWTLVQ TVLLPVIIGL
 VLRVFLNKWI DKILPILPYL SILGIGGVVF GAVAANAERL VSVGLIVFVA VIVHNVLYGV
 VGYLTGRV

> RXA02422 (1-435, translated) 145 residues
 VSTLISEPEV DKLRKRAKRS RRTIEWLAAA LLAPNLLLLA IFTYRPLLDN FRLSFFNWN
 SSPTSTFIGF DNYVEFFTRS DTLQVVLNTV IFTACAVIGS MVLGLLLAML LDQKLFGRNF
 VRSMVFAPFV ISGAAIGGAF QFVFD

> RXA02438 (1-759, translated) 253 residues
 MTDLIQLREV SKKYGAFQAL NDINLNVVAG EVTCVLGDNG AGKSTLIKIL SGLHPATSGE
 VIVAGDVVNF GSPRDALDAG IATVYQDLAV VGQMSVVRNF FLGQELTGRF GVLKQEEEMRR
 ITDEQLREMG IELRDVDVPV ASLSGGQRQV VAIARAIYFG ARVLILDEPT AALGVKQSGM
 VLRFIAAARD RGIGVIFITH NPHHAYLVGD HFILLNLGKQ VMDKSRAEVE LEELTLAMSG
 GGELDSLSE LKR

> RXA02439 (1-1023, translated) 341 residues
 MTKIKSGEAS TSIVERALKR PELTSLLGAV LVFTLFMVVA PAFRSWDSMA TVLYASSTIG
 IMAVAVGLLM IADEFDLSTG VAVTTAALAA SMFSYNLWLN TWVGALIALV ISLAIGFFNG
 FLVVVKTIAS FLITLATFLM LQGINLAVTK LISGTVATPT IADMEGFPSA RAVFASSIPI
 FGVNIRITVF WWLLFVIVGT FVLFKTRIGN WIFAVGGDEE AARAVGVPVR GVKIGLFMFV
 GFAAWFVGMH NLFLFDSIQA GQGVGNEFLY IIAAVIGGIS MTGGRGTVVG TMIGALIFGM
 TNQGIVYAGW NPDWFMFFLG GTLLLAVLLN HRFERFNKER S

> RXA02441 (1-657, translated) 219 residues
 MAELSVRNLT CTYGNHIALN NITARFPTGK ITALIGSNGS GKSTLLETIA GMLAPRSGSI
 NNLVPEIAFV PQRSHVSHNL PITIROTVSM GRWSAKKNWQ RLTAADCNIV DSCLDRLAIS
 GLADRPLGEV SGGQRQRALI AQGLAQQAPL LLLDEPLAAV DSHAASLIED VINQQRNQGT
 TIILATHDLD QAHQADQIIA LEKGIKPKR KATESIKKR

> RXA02442 (1-849, translated) 283 residues
 MKFFTDALIV PFDVSFISRA LVAGCLAAIL CSLIGTWVIL RRLTFFGDAM SHGLLPGVAT
 ASLLGGNLMF GAAISALIMS AGVVWTSRKS SLSQDVSIGL QFITMLSLGV VIVSHSDSHA
 VDLTSFLFGD ILGVRPSDIF IIAIATVLGG LTIFLFHRQF TALAFDERKA HTLGLNPRFA
 HLLMLALIAL ATVVVSFQVVG TLLVFGLLIG PPATAALLVQ DKASISLIMI VASLLGCAEI
 YLGLLISWHA STAAGATITL LSAAIFFATL LTKSAISRLN FTA

> RXA02447 (1-270, translated) 90 residues
 WWWLAEIIPV RMKGIGTGIS VFCGWINGV LALFFPALVS GVGITFSFLI FAVVGVIALA
 FVTKFVPETR GRSLEELDHA AFTGQIFKKA

> RXA02451 (1-1524, translated) 508 residues
 MNTDTTQDGV SPEPSDPHLG SEVAETHREK KFFGQPWGLA NLFGVEMWER FSFYGMQSIL
 AFYLYYSVTD GGLGMNQTAAL LSIVGAYGGF VYMTSLVASF IADRVLGSER TLFYSIIIVM
 LGHIALALIP GYTGLSIGLV LIGLGGGGV TAAQVVLGQL YSRDTRRDA GFSIFYMGVN
 LGGLFGLPLT NALGWGGGFH WGFIAAVGM ALGLIQYVAM RKTITGAAGH TVPNPLPKNE
 YARWIIGAVV VVAAVVALIA TGIKLEWLS NITAAIALIA AIALLAQMYV SPLTTAAEKS
 RLLGFIPMEI GGVLFFAIFQ TQFTVLAVYS DTRLDRNFFG IDLPPGLINS FNPIFIIFIS
 GIFATLWTKL GAKQWSTAVK FGVANIVIGC ALFFFLPFAG GAENSTPMAL IIVVYFLFTI
 AELLSPVGN SLATKVAPEA FQSRMFAVWL MAVSMGTSLS GTLGGYYDPT DAGSEKVFPI
 TVGVAAIVLG AIVIAAKGWV LKKFIDVR

> RXA02491 (1-1254, translated) 418 residues
 MRVAMISMHT SPLQQPGTGD SGMNVYILS TATELAKQGI EVDIYTRATR PSQGEIVRVA
 ENLRVINIAA GPYEGLSKEE LPTQLAAFTG GMLSFTTRREK VTYDLIHSY WLSGQVGWLL
 RDLWRIPLIH TAHTLAAVKN SYRDDSPTPE SEARRICEQQ LVDNADVLA VNTQEEMQDLM
 HHYDADPDRI SVVSPGADVE LYSPGNDRAT ERSRRELIGP LHTKVVAFVG RLQPFKGPQV
 LIKAVAALFD RDPDRNLRI ICGGPSGPN TPDTYRHMAE ELGVEKRIRF LDRPPSELV
 AVYRAADIVA VPSFNEFGL VAMEAQASGT PVIAARVGGL PIAVAEGETG LLVDGHSPHA
 WADALATILD DDETRIRMGE DAVEHARTFS WAATAQLSS LYNDIAIANEN VDGETHHG

> RXA02507 (1-1401, translated) 467 residues
 MSEQLQGVTH SESTPGKTPK RAALSSWIGS ALEYDFAVY GTAAALVLNH LFFPADTSPG
 IAILAAMGTG GVAYVVRPLG ALIMGPLGDR YGRKFVLMC LFLIGASTFA VGCLPTFDQV
 GYLAPALLVL CRVIQGLSAS GEQSSAISVS LEHADERHRA FTASWTLHGT QFGTLLATGV
 FIPFTLFLSE DALMSWGWRV PFWLSAAVVL VAFLIRRGLE EPPAFRENKE AVAGAASPLA
 MTLRYHKAHV ARVAIAAMIN SVNIVFTVWA LSFATNIVGL DRSTVLLVPV VANLVALIAI
 PLSGMLADRI GRRPVFIMGA IGGGLAMNGY LGAIYSGNWT MIFFMGVLM GLLYSMGNV
 WPAFYAEMFP TSVRVTGLAL CTQIGFAVSG GFVPVIASAL AGDQGDQWMK VSIFVGVVCV
 ISALVAMTAK ETKALTLDEI DALHTAGGEA ADLAAASKAS EAQLAAQ

> RXA02515 (1-756, translated) 252 residues
 MSTLEIRNLH AQVLPSDESA EPKEILKGVN LTINSGEIHA IMGPNNGSKS TLAYTLGGHP
 RYEVTAGEVL LDGENILEME VDERARAGLF LAMQYPTIIP GVSVANFLRS AATAIRGEAP
 KLEWVKEVR TAQEALAIIDP EFSNRSVNEG FSGGEKKRHE VLQDLCLKPK FAIMDETDSG
 LDVDALRIVS EGINSYKQET EGGILMITHY KRILNYVKPD FIHVFANGQI VTTGGAELAD
 KLEADGYDQF IK

> RXA02562 (1-720, translated) 240 residues
MFLTQVSLLD HPESLPGYLS SLAIVEYLHE QPLEFRAPIT VITGENGVGK STLVEALAVG
MRLNPSGGSR HANFGREGDI VSSLHQSLKL VRRENPRDAF FFRGETMYNV ASYYEELMGE
KNMHDHLHKMS HGESVFAVID RRFNNQGGFFV LDEPEAGLSM LRQLELLGKL GNLARGGAQI
IMATHSPILL AIPGAEILEI TSSGVAKVNF EDAAEAVRAAR EFVADPRGTA AFLTAEEDHQ

> RXA02595 (1-651, translated) 217 residues
VIVVAMASIM ACLKAARLNN PMKILLCLWR DTTHPQGGGS ERYLERVGEF LADQGHEVVF
RTAGHTDAPR RSFRDGVRY SSGGKFSVYP KAWVAMMLGR VGIGTFKVD VVVDTONGIP
FFGKFFSGKP TVLLTHHCHK EQWPVVGRVL AKVGWLIQS IAPRAYKTAP YVTVSEPSAE
ELIALGVDDQ RIHIVRNGVD PVPLHTPKLD RDGQHAV

> RXA02597 (1-1788, translated) 596 residues
LPEQDLTTLA NDWLQAFEKA TASSSPDEAA TAVVQLFEDE GYWRDLLAFT WNLTTAEGAD
EIAEMIRNTW PSSIFRNV EL KGEPADEGDG VTRVHFSCS ADFKCTGIVR LRNGKAWTLL
TSARELLEHP EPKGRNREM VVHGQNE DTR NWTDRKNDRQ AALGVTEQPY TLIIGGGQGG
IALGARLKRL GVPALIIDKA SRPGDQWRSR YHSLCLHDPV WYDHLPIYPF PDHWPVFTPK
DKMGDWLEHY VGIMDLDYWT NTECLRASYN EDTKQWDVTV NRDGAESTLH PTQLVMATGM
SGSPNKPTLP GQDKFQGEIR HSSEHPGGDV DRDKNVVVLG ANNSAHDICA DLYSNGAKPV
MIQRSSTHIV RSDSLMREVF GLYSEDAVE AGIDTDADL LFASWPYKVL PGVQKQAFDK
IREDDKEFYD KLENAGFLD FGDDDSGLFL KYLRGSGYY IDVGASELVA DGKIPVRSNV
SIEDVKENSV VLTDTGTELP DVIVLATGYG NMNNWVAQLV DQETADKVG CWGLGSETTK
DPGPWEGELR NMWKPTNVDS LWFHGGNLHQ SRHYSRYLSM QLKARYEGMN TPVYSK

> RXA02605 (1-495, translated) 165 residues
VACPWAGTAA LNLAAKHPDQ FRQAMSWSGY LNTTAPGMQT LLRVAMLDTG GFNVNAMYGS
IINPRRFEND PFWNMGGLAN TDVYISAASG LWSPQDDGVR VDHRLTGSVL EFVAMTSTRI
WEAKARLQGL NPTADYPMY IHWGWAQFNSQ LERTQGRVLD VMNAW

> RXA02614 (1-729, translated) 243 residues
MTATLSLKPA ATVRGLRKS Y GTKEVLQGID LTINCGEVTA LIGRSGSGKS TILRVLAGLS
KEHSGSVEIS GNPVAFQEP RLLPWKTVD NVTFLNRTD ISWSEAQERA SALLAEVKLP
DSDAAWPLTL SGGQAQRVSL ARALISEPEL LLLDEPFGAL DALTRLTAQD LLLKTVNTRN
LGVLLVTHDV SEATALADHV LLLDDGAITH SLTVDIPGDR RTHPSFASYT AQLLEWLEIT
TPA

> RXA02616 (1-711, translated) 237 residues
LQKHTRGGKH RKQTTSPVTK GGVAFAVAT GAVSTAGAGG AVAAQASNQP VEVNFELTAN
DTTDLVAGSS APQILSIAEF KPVVNLGDQI VKTIQYNADR IQADLDARGP SVVRPAEGSY
TSGFGARWGT NHNGVDIANA IGTPILAAMD GTVIDAGPAS GFGNWWRLQH EDGTITVYGH
METVEVTVGQ TVKAGERIAG MGSRGFSTGS HLHFEVYPAG GGAVDPAWPL AERGITL

> RXA02627 (1-843, translated) 281 residues
DVTVESQPER VVALGWGDAE AALEFGVQPV GASDWLAFGG EGVGPWIEDS AYDEAPEIIG
TMEPEYEKIA ALEPDLILDV RSSGDQERYD KLSSIALTIG VPEGGDSYLT PRAEQVTMIA
TALGQAERGE EVNAEYEQLT ADIRAAHPGW PEKTAAVSA TATSWGAYIK GSNRVDTLLD
LGFQENPELA KQQPGDTGFS IKFSEETFGV VSDSLVVGFA IGMTPEEMAE QVPWQMLTAT
RDGRSFVMPE EISNAFSLGS PQSTRFALDA LVPLLEEHA G E

> RXA02628 (1-405, translated) 135 residues
MLEGFRDFVL RGNVIELAVA VVIGTAFTAI VTAFSESIIN PLIASIGSTE VEGLGFHIRA
GNAATFVDFG AVITAAINFL IIAAIVYFVL VAPMNKLSET LAKRKGVEED ETPASIEAEL
LTEIRDLLQE QKRLQ

> RXA02650 (1-579, translated) 193 residues
MVNVTSKDAG ANVTPMSKKE KRRTVKQVVA LMAAIVVVIA SLDQIVKQIM LSWLEPGVPV
PIIGDWFRFY LLFNPGAAFS MGENSTWIF TTIQLSFVIG IAIYAPRIKH KWIAAGLALV
AGGALGNVLD RLFRDPSFFF GHVVDYISVG NFAVFNIAA SISCGVVVFL IGMFLEDREN
AQHAKATDEK DEA

> RXA02660 (1-639, translated) 213 residues
 MIIGVTLLVF IVMSFSPADP ARLALGESAS PEALEAYREA NGLNDPMMVR YFDFILGMLK
 GDGLTSSGGV AVTDIVARAF PITLQLTFWG LIIAVVVALI LGVIAALYRD RWPDQLIRVV
 SIAALATPSF WLAILLIQWL GTIPGAWGFF PALVTRWVPF SEDPATYFNN IALQRLRWQS
 PLQVLWPALE VPPWWKNWTR TTSQQSVQD PQN

> RXA02661 (1-219, translated) 73 residues
 VIGLRVGLSM GGAVIIEIIF NIQAMGQLIL DGVTRNDVYL VQGVTLTVAI AFIIIVNIAVD
 LLYVLVNPRI RSI

> RXA02663 (1-1395, translated) 465 residues
 MAPILVFATV LVADAIVFEA SLSFINAGVK PPSPSWGNIL ADGKALLLSG AWWPTFFPGL
 MILLTVLCLN ILSEGLTDTL ASPKPKPVS AKAALKKEE SGEKEGSGIV LGHTTREETAN
 ASLLASLAAL STSENNNSNNR LIFDGNPTPL LEVRDLKISF PNAHGDNINIV DGVNFTVAPG
 QTMGLVGESG CGKSITAMSI MGLLPPTAKI EGEILFDGKN LLDLKPDELN ALRGHEIAMI
 YQDALSSLNP SMLISAQMKQ LTRRGGRSA EELLELVGLD PKRTLQSYPH ELGGGQRQVR
 LIAMALTRNP RLLIADEPTT ALDVTVQQQV VDLLNELREK LGFAMIFVSH DLALVARLVH
 KLTVMYAGQV VEQGTREIL IDPRHEYTRG LLGSVLSIEA GVDRLYQVPG TVPSPKEFVA
 GDRFAPRSEF PELGLDQKPV LRPITGTEHA YAATDELLAA KGEQR

> RXA02664 (1-660, translated) 220 residues
 VGESGCGKST LARVMVGLQP VTSGEVLFGK KPMKPRGAQR KELGSSSVSVV FQDPATSLNP
 RMTVREQLLD PLRVHKGVD ASRNQWVSEL ISMVGLPQSA LEVLPRQVSG GQRQVRVAIAR
 ALALKPDIIIV ADEPTSALDV SVRAQVLNLL LDLKTELGLG LVFISHDINT VRYVSDRIAV
 MLAGEIIEEN TTSEIFNNAQ QDYTRTLLEA TPSSLNKTRL

> RXA02684 (1-864, translated) 288 residues
 VLAUGLVLVF VVTWADSKL NRVDATPATQ VANTAGTNWL LVGSDSRQGL SDEDIERLGT
 GGDIGVGRD TIMVLHMPRT GEPTLLSIPR DSYVNVPGWG MDKANAAFTV GGPELLTQTV
 EEATGLRIDH YAEIGMGGLA NMVDAVGVE MCPAEPMYDP LANLDIQAGC QEFDGAALG
 YVRTRATALG DLDRVVRQRE FFSALLSTAT SPGTLLNPFR TFPMISNAV GTFVGEHGHV
 WHLARLALAM RGGIVTETVP IASFADYDVG NVAIWDEAGA EALFSSMR

> RXA02728 (1-813, translated) 271 residues
 MAIVSLDNVT VSIEGKKLLD AVSLKAYPGE VLGLIGPNGA GKSTLLSVLS GDRLPDSGEV
 NVGGLDPATA AASDMARVRA VMLQDVSVAF SFLVWDVDEM GRRPWQKAST PEEDHEIIEA
 ALAATSVSHL AEREITTLTG GERARVALSR VLAQQTPIVL LDEPTAAMDI SHQEQTGLTA
 RALAAAGAAV IVVLHDLNAA AAYCDSIVCL SDGRVIASGS VDQVYSTETL SRVYGWPIRV
 DHSGKYVRVE PDRSEANLPS VLQVKNVSP A

> RXA02750 (1-816, translated) 272 residues
 MAVLFSIMGA LILLVLYLVF LGKLQIDGLM VDLPSARD D VEGFVFNWVF SGILITSAIT
 VPQAALGVLV EDRTGGIKD FLVAPVSRTT LTVSYIFAAV IVAMTILIFE IVVGSIGLAI
 LGHFMSIAR VLELVVALL LTLVFSIAIA FLITLVKSQG GMSALSSLVG TLAGFLSAAY
 IPPIALPEAV TNVLNLFPLFT PAGMLIRQIV VAPALDAISL PPEAFDIFQF GYGLKLEMFG
 EPVSTWVAVG IVASWGVVFG LIAAFKMKSV VR

> RXA02761 (1-201, translated) 67 residues
 MMDGINRRRT LITGYSLTTI SHVLIGIASV AFPVGDPLRP YVILTLVVVF VGSMQTFLLG
 SYLGYAL

> RXA02762 (1-285, translated) 95 residues
 MLSELFPLAM RGFAIGISVF FLWIANAF LG LFFPTIMEAV GLTGTFMFMA GIGVVALIFI
 YTQVPETRGR TLEEIDEDVT SGVIFNKDIR KGKVH

> RXA02769 (1-711, translated) 237 residues
 TVVPVYLAEL APLEIRGSLT GRNELAIVTG QLLAFVINAL IAVTLHGVID GIWRIMFAVC
 ALPAVALFLG MLRMPESPRW LVNQGRYDDA RRVMETVRTP ERAKAEMDEI IAVHSENNAA
 LPGVKQSSGQ ASGQVSSKHT HMSIGEVL SN KWLVRLLIAG IGVAVAQQLT GINAIMYYGT
 RVLEESGMSA EMAVVANIAF GAVAVIGGLI ALRNMRLDR RTTFIIGLSL TTFHLL

> RXA02795 (1-1095, translated) 365 residues
 IDVSLPERTA SAYPHELSSG QRQRALIAM LANDPDLIC DEPTALDVV VQKQIVDLLL
 RLTKERGTA LFITHDLGLI ARTCERLLVM KSGETVERGD TEAILRSPAH SYTQQLLDAS
 ILDQPEIASD SGAPVVIDVE EASKSFKETT ALHKVSLAVR KGDLLGIVGG SGSGKTTLLK
 LIAGLDKPTT GTVAVTGGVQ MVFQDPQSSL NPRMKIKDIV AEPLLGWNAE EKTTRVAEVI
 TQVGLSPDVL DRYPHEFSSG QRQRISIARA LAIKPAILLA DEPVSAIDVS VRKQVLDLLQ
 QLVEEYGITL VEVSHDLAVV RHLCTTVWVM EQGRVLEQGP IDSVYDHPQT EYTKELLDVAV
 PRLSL

> RXA02808 (1-258, translated) 86 residues
 FYFGILPVLA ESASHFGIEP VEMARASITG QPVHMQSPLV PAILLLVSLA NVNLGDHKKK
 VLWRACIVSI AMLAVALFIG VVPLSA

> RXA02863 (1-975, translated) 325 residues
 MKKSLIAIVA SALVLSGCTS DSSDSSGTSG TVETTSITTS VAAADGAFPR TVTLDDSSIT
 LESKPERIAV LTPEAASLVL PITGADRVVM TAEMDTADEE TAALASQVEY QVKNNGSLDP
 EQVVAGDPDL VIVSARFDTE QGTIDILEGL NVPVVNFSD AWGDIDAITK HLEIVGELVG
 EEDKAAEAIA EIDANRIDID KPATSPTVLT LMQRGPRQMV MPESAMLNGL IREAGGTPVV
 DSLGAVGTIT ADPEQVVAMA PEIIIIQDFQ GKGRNFANF LSNPALANVP AIENDKIFYA
 DVTVTGVTAG TDITGLQOV AEMLS

> RXA02864 (1-780, translated) 260 residues
 MPQLVEIRDL NVEFPSRHAV KNVSFSAPAG KVTALIGPNG AGKSTALSAI AGLVESTGEV
 MVGGSGVASK SAKARARLLS LVPQNTLRI GFSARDVVAM GRYPHRGRFA VETDADRRAT
 DDALRAINAI DIAEQPVNEL SGGQQQLIHI GRALAQDTAV VLLDEPVSAI DLRHQVEVLQ
 LLRARANSCT TVIVVLHDLN HVARWCDHAV LMADGEVVSQ GDIREVLEPA TLSTVYGLPI
 AVRDDPETSS LRVIPHPNPF

>RXN00001 TRANSLATE of: rxn00001.seq check: 7420 from: 1 to: 1128
 MATVTFKASLSYPGAKEPTVKKFNLEIADGEFLVLVGPSCGCKSTTLRMLAGLENTVDG
 AIFIGDKDVTHVAPRDRDIAMVFQNYALYPHMTVGENMGFALKIAGKSQDEINKRVDEAA
 ATLLGLETFLEKPKKALSGGQRQVRAMGRAIVRNPOVFLMDEPLSNLDAKLRVQTRTQIAA
 LQRKLGVTTVYVTHDQTEALTMGDRIAVLKDGYLQOVGAPRELYDRPANVFVAGFIGSPA
 MNLGTFSVKDGDATSGHARIKLSPETLAAMTPEDNGRITIGFRPEALEIIPGESTDLISI
 PIKLDVFEELGSDSFLYGLVGEGLGSSSEDVPESGQIVVRAAPNAAPAGSVFIHARIV
 EGGQHNFSASTGKRLP

>RXN00099 TRANSLATE of: rxn00099.seq check: 3872 from: 1 to: 1173
 VKNPRLIALAAIILTSFNLRTAITALAPLVSEIRDDLGVSAALIGVLGMIPTAMFADAAAF
 ALPSLKRKFSTTSQLLMFAMLLTAAGQIIRVAGPASLLMVGTVFAMFAIGVTNVLLPIAVR
 EYFPRHVGGMSTTYLVSEFQIVQALAPTAVPISQWATHVGLTGWRVSLGSWALLGLVAAI
 SWIPLLSLQGARVVAAPSKVSLPVWKSSVGVLGLMFGFTSFATYILMGFMPPQMGDPQL
 GAVLLGWWSILGLPLNILGPWLVTFTNCFPMVVIASVMFLIGNGGFCLAPDVAPWLWAT
 LSGGLPLAFPMALTINIRAETSAGASALSSFGQLGYTIACFGPLLTFGFIVDATGSFRT
 IFVLFAVATLTVIRGGYFATRQVYVEKLLNR

>RXN00193 TRANSLATE of: rxn00193.seq check: 1918 from: 1 to: 594
 KAFXQREGFISAFGFTVLVVIVSVITVNIFAFLLAWLLTRKLRGTNFFRTVFFMPNLLIG
 IVLGYTWTMINAVLSHYATTISADWKFGYAGLIMLLNWQLIGYMMIIYIAGLQNVPPPEL
 IEAAELDGVNKEWMLRHVTIPVMPSITICFLTLSNSFKLFDQNLALTNGAPGGQTEMV
 ALNIINTLFNRMNVEGVG

>RXN00378 TRANSLATE of: rxn00378.seq check: 9591 from: 1 to: 2610
 VDKAVNTAISDAKTAALKAGVGLNRATASEEEEDLSSSIKVSLAFELEGLSNAPSIMVVE
 KALEKIPGVSADLIYPSQTAWITATDRVHPETLIEVFEQFGIKAHLNSNSSLRRHQQLSA
 EVNREARLDYRSMRMDAKRISPRVRRHNRQEMVHAVRARESGWIKRRNHTTSQHEDPSG
 DVLFTRALITPKRLWVSLPFALIVLALSLSNPWFQFDYQWLSAVLAIPVVVWGAWPFHR
 AAAGGIRRGISALDATSSIAIAAAYAWSIAMLLFETPGGKSWSYPSWFAFDHGTLTQNE
 IYFDVACGITVLLLAGRLLTRRRSQSSLLAELGRQLIDPQRIVTVVRKHRLKRVVQELNI
 PVQEVVRNDDVKVPNTTIPVDGTVIGGGSRIAASIIMGQDQRDVKVNDKVFAGSLNLES
 EIKVRVIRTGHRTRIAAVHRWVKEATLKENRHNRAAIRSAGNLVPITFTLAVVDFCLWAL

ISGNINAAFTTTTFLAVLACVAPVALALSAPLATRNSIEAAARHGILVRSGEIFRVLDDVDVT
AVFNVRVGTLTLDGEMTVETVTADKGEDPELVLRVAGALAMESHHAISKALVKASREARDTG
AGGEDVPHWIEVGNVEITEAGSFQATIELPLIKPSGEKIMRTTEALLWRPRSMTEVREHL
SPRLVAAATSGGAPLIVRWKGKDRGVITLSDHVRSDSSDAIAIEEQGIETMMLSRDTYP
VARRYADSLGITHVLAGIAPGKKAQVVRVAVHTRGSTVAMIGDESVMDCCLKVADVGVLMGV
DRPSDLRDDSDDPAADVVMREEVMSVPTLFLKLARRYAKLVNGNIALAWIYNGVAMVLAV
SGLLHPMAATVAMLASSLLIEWRSGRARKY

>RXN00412 TRANSLATE of: rxn00412.seq check: 7568 from: 1 to: 1080
VSHTASTPTPEEYSAQQPSTQGTRVEFRGITKVFSSNNKSAKTTALDNVTLTVEPGEVIGI
IGYSAGKSTLVRLINGLDSPTSGSLLNGTDIVGMPESKLRKLRNIGMIFQQFNLFQS
RTAAGNVEYPLEVAKMDKAARKARVQEMLEFVGLGDKGKNYPEQLSGGQKQRVGIARALA
TNPTLLLLADEATSALDPETTHEVLELLRKVNRELGITIVVITHEMEVVRSIADKVAVMES
GKVVEYGSVYEVFSNPQTQVAQKFVATALRNTPDQVESEDLLSHEGRLEFTIDLTETSGFF
AATARAAEQGAFVNIVHGGVTTLQRQSFSGKMTVRLTGNTAAIEEFYQTLTKTTTIKEITR

>RXN00431 TRANSLATE of: rxn00431.seq check: 340 from: 1 to: 789
MVSIDTYNACVDFPIFDAKSRSMKKAFLGAAGGAIGRNQDNVNVVEALKNVNLHLREGDR
VGLVGHNGAGKSTLLRLLSGIYEPTRGSAIRGRVAPVFDLGVGMDFEISGYENIIIRGL
FLGQTRKQMKAKMEEIADFTELGEYLSMPLRTYSTGMRIRLALGVVTSIEPEILLDEGI
GAVDAAFMAKARDRLQALVERSILVFASHSNDFLAQLCNTALWVDHGQIREAGLVDPDV
EAYEGKGAGDHVRRLLTRMEEEE

>RXN00444 TRANSLATE of: rxn00444.seq check: 7535 from: 1 to: 837
MVLAQTKKARRSENHILPGWLLIPATLAMLLIIGPIFALLLQIPWDRSWELLTAPESLGT
ARLSIGTALFSTALCAIVGFPLALALHLYERSHPRVTSVLTVLVYAPVLSPVVSGLALT
FLWGRRGFLGSLWDQVGLPIAFTTTAVVFAQVFVALPFFISTVTTALRGIPKQFEEIAAT
EGATRWEIMHKMIIPLAMPGIFTGMILGFARALGEYGATLTFAGNIAGVTRTIPLHIELG
LSSNDMDKALGAVIMLLAVVLIIGAIGALRLFSKVRKV

>RXN00466 TRANSLATE of: rxn00466.seq check: 8825 from: 1 to: 996
VQSRLSKILRSSVVGAVLALLAGCSNNADDDADSTSTGNSAFPVSIHEFGTTTTIDDV
PERVVTLGVTDADIVLALGTVPGVNTGYKFFENGLGPWTDDELVEGKELTLSDSDSTPDLE
QVAALEPDLIIGVSAGFDDVVYEQLSDIAPVVARPAGTAAYAVAREEATNLVARAMGQSE
KGQELNEETDALIQAARDENPSFDGKTGTVILPYQGGYAYLPGDARGQFLDSLGLISLPE
AVLSRDTGDSFFVDVPAESVKDVGDDVLLVLSNDENLDITAENPLFETLNVVQKDAVIVA
TTEERGAITYNSVLSVPFALEHLAPRIAEALK

>RXN00523 TRANSLATE of: rxn00523.seq check: 9218 from: 1 to: 1026
MSLSHQLKRQRASRNSRRWLIVAALGVVTLGIFAFSLMWGEVIFYGPAQVLKVLSGQQVPG
ASYSVGVRLRLPRAVMGLTAGLAFGAAGVIFQTVLRNQLASPDIIIGISSGASAAGVICIVF
FGMSQSAVSAISLCASLAVALLIYLVAYRGGFSATRLILTIGIGIAAMLNSLVSYLSKAD
SWDLPTATRWLTGSLNGATWDRAMPLIVTTVVLIPLLVANARNVDLMRLGNDASVGLGVA
TNRTRVIAIIAAVALIAVATAACGPFAFVAFVSGPIAARILGSGGSLIIPSALIGGLIVL
IADLIGQYFLGTRYPVGVVTGAFGAPFLIYLLIRSNRAGVTL

>RXN00525 TRANSLATE of: rxn00525.seq check: 5915 from: 1 to: 1263
MSLAESILLALTSLRSNKMRAILLTLLGVIIGIASVIGILTIGKALQDQTLNSLES LGAND
LSAQVEERPDEDSPEPDMFAFSGAANSSGNLIPEETVDTLRDRFAGSITGISVGGMGTOG
TLIGDTADLKSDLLGVNEDYMWNGVEMNYGRAITQDDVAAQRPVAVIAPDTFNTLFDAN
PNLALGSEVAFELNGQETFLRVIGVYKEAAAGGLVGSNPTVHTYTPYTVANDITHTEDGL
NTLSIRAAQGVDDQSLKGS LQTYFDALYANND SHHVAMLD FRKQIEEFNTILGAMSLGIS
AIGGISLLVGGIGVMNIMLVSVTERTREIGVRKALGARRRDIRLQFVVEAMIICFIGGIL
GVLLGGILGLIMSSAIGYISLPPSLSGIVIALVFSMAIGLFFGYYPANKAAKLDPIDALRY
E

>RXN00702 TRANSLATE of: rxn00702.seq check: 9529 from: 1 to: 1707
MSAPFSARTAWSTDPVLELESVAASYDDERTLAAPQISDVNLTLEFEGEILLVVGRTGSG
KSTLLNAMSGAMPHATGGRLDGRVRVVGDRDTRDFPPRMLSDVVGVVGQDPAASFITNTVE
EELAYSMEQLGLPPAVMRKRVEETDLLGIAELRYVPLAELSGGEQQRVAIGAVLTTRPA
LIILDEPTSALDPNGAEDVLATVTKLAHDLAMTVVLAEHRIERVLYQVDRVAHVADGHV

TVGTPEEIMADSDVAPPVELGRWAGWAPLPLSIRDARAHSADMRKRLYQRGLVVNKLHN
HAYQPLLIAEDIMVDFPEIRAVDGVNLSNSGEITVLMGRNGCGKSSLLWALQSGSTRNQ
GSVQVLDEAAGFSWTDPKTLKPAKRRNLVSMVPQTPTDILYESTVHAELARSDKDAAPA
GTTREILDSLVPNIPDHLHPRDLSEGQKLSLALSQQLAAKPRVVFDEPTRGLDYDGKKS
LARSFQQLADDGHAILVVTHDVEFSALCADRVLFMASGKIISDGTAVEILPASPAYAPQV
AKITAGIQEESHWLTVSAVKAALGHGEIS

>RXN00726 TRANSLATE of: rxn00726.seq check: 2288 from: 1 to: 591
NAGRLYVDGDLIGYRERDGVLYEISEKDAKQRSDIGMVFNFNLFPHRTVIENIIEAPI
HVKKQPESKARARAMELLEQVGLAHKADAYPVQLSGGQQQRVAIARAVAMEPKMLMFDEP
TSALDPVELVGEVLRVMQLADDGMTMLVVTHEMGFAHEVADQVVFMDAGVVVEAGTPEQV
LDNPKEQRTKDFLSSLL

>RXN00732 TRANSLATE of: rxn00732.seq check: 6509 from: 1 to: 1647
NHLALLPTVKADIIDNGVVTGDIGYIWHGTGGIMLALTLVQVACAIAGVYFGSKLSMRVGR
DLRSAIFGKVVNFSEEMGQFGAPSLITRNTNDVQQVQMLVQMTSTIMISAPMLAIGGII
MAVRQDLGLSWLMVVSIPVLIIVVALIIVRMVPLFQTMQKRIDRINQIIREQLTGIRVIR
AFVREDVERERFTTASKDVAIDIGVRTGNLMALMFPAVMLIMNLSAVAVIWFAGFQVESGE
TQIGTLFAFLQYIMQILMGVMAAFMFVMVPRAAVSADRIGEVLLETTPSVQAPETPAQPS
TSAGEIVFNATFAYPGADDPVLNNVSFRVAPGSTTATIGSTGSGKTTLIGLVPRLFDVT
EGDVTVDGTDVREPLKLWDRIGLVLPQKSLFSGTIANLRYGNEDATETQLWQALIAIA
QAADFVREMPEGLDSEIAQGGTNVSGGQRQLAIARALLKQPEIYIFDDSFSLADVSTDA
ALRRALSTNLPDATKLIVAQRVSTIRDADQIVVLDNGEVVGIGTHTNLLNTCGTYREIVE
SQETAQAQS

>RXN00759 TRANSLATE of: rxn00759.seq check: 3116 from: 1 to: 924
MLRYVGRRLQLMIPVFFGATLLIYALVFLMPGDPVQALGGDRGLTEAAAAEKIRQEYNLDK
PFIVQYLLYIKGIFVLDFGTTFSGQPVIDMARAFPVTIKLAIMALLFESILGIIFGVIA
GIRRGGIFDSTVLVLSLIVIAVPTFVIGFVLQFLVGKVGWGLLPVTVGSNTSITALIMPAV
VLGAVSFAYVLRRLTRQSVSENLRADYVRTARAKMSGFNVMNRHVLNRSLIPVATFLGAD
LGALMGGAIVTEGIFGINGVGGLTYQAILKGEPTTVVSIVTVLVIVYIIANLLVDLIYAV
LDPRIRYA

>RXN00808 TRANSLATE of: rxn00808.seq check: 7354 from: 1 to: 1458
VLGTNVFGALAVMLFVRFLIPQPDASNFAEISYLPVAGFAYLAFAIVAGMLVTFMFRP
VLDWQRSPEDHDRNMVRNLVMRIPIYQAILCAVWVLIGIAIATLISASVSTSLALVVAFS
TLMAAAIVVLLTYLEAERLVRPVAASALARREFDSTLEPPVSQRLRMTWLLTLGIPVMGI
LLLIWGYSGGIFGSDASGIMPAIALAFASLVGTGYNLRLVVSSVVDPIRELQEAIRNRV
RGENDVQVDIYDGESEIGVLQAGFNEMMRGLRERQVRDLFGRYVGAEVAKRALEERPTLG
GEDRKVAVLFVDVIGSTTFVAVNHTPEEVVEALNEFFEHVVEVVHRNKGVINKEFGDAALA
IFGAPLPLSDATGHALAAARELRAELKDLQLKAGIGVAAGHVAVAGHIGGHARFEYTVIGD
AVNQAAARLTEIAKTTTPGRTVTNASTLREANEAEQARWTLMKSVELRGRSQMTQIARPIRP
TLADRS

>RXN00828 TRANSLATE of: rxn00828.seq check: 8544 from: 1 to: 453
VRGGLNTPPHKWSADLAARIGTVFQDPEHQFVARTVRDELEIGPKIMKVDASERIEELL
DRLRLRHLENANPFTLSGGEKRRLSVATALVAAPKLLILDEPTFGQDPETFTELVTMLRE
LTDNGISIVSVTHDPDFIAALGDHHEIVSAK

>RXN00832 TRANSLATE of: rxn00832.seq check: 2297 from: 1 to: 1050
MPFSWLKPIDYARIFVGWASIFIPLITLPSIIEALALIVAVILFCAFGVVKMAERLAHIL
GDPFGSLILTLISIVIIEVILICAVMLGPADSTTAGRDSVMAVSMIIMGLVVGLCLLIGGL
RHGSMPHNGVGTPTYLVLIATFSVIAFAVPAFRGEYSTGQALVISTLTAVVYGFFLFRQM
GAQAGEFQEEVEVAEKADDAKWEVPFRGLILITVLPVLLSHDMATVMDEVLASLGAPV
AMAGLIIATIVFLPETITSLKAAWTGEIQRVSNLAHGAQVSTVGLTIPAVLVIGVITGQD
VVLGETPINLLLLGTTIAVTAIAFSSKKVSAVHGSVLLMLFGVYMMSMFA

>RXN00934 TRANSLATE of: rxn00934.seq check: 9723 from: 1 to: 1083
VRIGMVCYPYSFDEPGGVQAHILDLARTFIAQGHEVQVLGPCSADTQVPDFVVRGGGSIPI
PYNGSVARLSFGPKMFKAVRTFLREGNFDVLHIHEPNSPSFSMAALRFAEGPIVATYHAS
SSGSKLLKAFLPVLSPMLEKVRAGIAVSEMARRWQVEQVGGDPVLIPNGVETSMFKAARQ

IEPNDPVEIVFLGRRLDESRKGLDILLRALTRLDLPFTCTVIGGGTPREVAGINFGVRVSD
 EEKAAAILGRADIYVAPNTGGESFGIVLVEAMAAGCAVVASDLEAFSLVTDSEAAQPAQVL
 FKGTGSADLAKKLQALIDDPSSRSTLIAAGLKRANAYDWSTVSTQVMAYETIAIDKVRLL
 G

>RXN00939 TRANSLATE of: rxn00939.seq check: 3908 from: 1 to: 1236
 MTRQKTQPFLEKFSKYYPGVMIAALAVGLITLNLVELALTLVLIACPGALVISIPVSIVA
 GIGRSKADGVLIKGGEYLETSAKVDTVVVDKGTGLTNGRPELTNVDVLDPAYSDDEVLTLL
 AARAETASEHPLAEAIIRGAENRGLTVAMVEKAEPVAGRGIRADVDGATVAVGSADLLDH
 TPDNTRILELNEQGRITAMYVINGKAVGIVAVADTIRDDAPAAIRSLHNKGIRVVMATGD
 AERVARNVAAELGVDEVRaelmpedkleivkelQAQGRVVAMVGDGVNDTPALATADIGV
 AMGAAGSPAAIETADIALMADKLPRLPYALGLAQRTVTRMVRNIGIALLTVTILLAGVLL
 GGVMTSIGMLVHEASVLLVIAIAMLLLRPTLKDCKADVSTADAAKETLSA

>RXN00960 TRANSLATE of: rxn00960.seq check: 4118 from: 1 to: 1035
 MARHCCSNRYASTVFSGLIAYGASQALYPWLLKDHQSVTEIDLADAGALQPYFNIEMPPPF
 EVMTALLLAFCLGLGMAVIKSDTLFKVTRELERVVMKTITAFVIPLELPLFIIFGIFLGMGM
 NGGLLEIMSAFGKVLILAVVGTLLFLAIQFIIAGAVSKKNPWKLFKNMLPAYFTALGTSS
 SAATIPVTYQQTLKNDVDVNVAGFVVPLCATIHLGASMMKIGLFTFAVVFMYDMEVGVGL
 SIGFLMLGITMIAAPGVPGGAIMAATGMLASMLGFNTEQVALMIAAYIAIDSFGTAANV
 TGDGAIAVIVNKFAGKQLHTTSPDEIEEDDRVAFDITPSDVEHHK

>RXN00980 TRANSLATE of: rxn00980.seq check: 2367 from: 1 to: 1794
 MLADAFMIAAAIVAGWPQIASAYQALRIRMVSIIDLLVVVAAVAGAMFINNYWESAAVTFLF
 ALGKALERATMNRTRKALSDLVDAAPETATRLNADDSTEVELWELEPGDIVLVRNGEQI
 PVDGNIAGVGGIDESNITGESMPAEKQGSDVYAGTWLRSGVLRVEATGIGSDSTLAKI
 IHRVEDAQDDKARTQTFLEKFSKWYTPGVMIAAAVVGLITWDVELALTLVIGCPGALVI
 SIPVSIVAGIGRAARDGVLIKGGEYLETAAKVDVVVDKGTGLTTGRPELTDVEVIEPAY
 SQGEVLELAARAETASEHPLADAIIRGAQDRGLSTTLVEAAENITGRGIIANVDGQAVAV
 GSAELLDHEPDSTRIELNAEGKTAMFVGNGHAIGIVAVADAVRSDSASAIESLHKAGI
 QVVMATGDAHRVAQNVASKLGVDEVYSELLPEQKLELVRDLQAAGKTVAMVGDGVNDTPA
 LAAADIGVAMGVAGSPAAIETADIALMADRLPRLAHAVTLAKRTVTRMIRINILIALATVM
 VLLAGVLFGGVTMSVGMLVHEASVLLVISIAMLLLRPTLKDAAQASDIKRSEIQQIA

>RXN01000 TRANSLATE of: rxn01000.seq check: 4854 from: 1 to: 846
 MSTLTSHRTVPAPSSPPARPKNLARNIVAIVAALIVLIATGTLKIEWNELPQMPAQVWHY
 LELMFSDPDWSKFGRAVQEMWRSIAMAWLGAILCVVSVPLGMLAARGVGPYWLRTVLRF
 VFAVIRAFPEVVIAIILLTVTGLTPFTGALALGISGIGQQAQWYEAIESTPTGPSEAVR
 AAGGTTPEVLRWALWPQVAPSIASFALYRFEINIRTSAVLGIVGAGGIGSMLANYTNYRQ
 WDTVGMILLIVVVVATMIVDLISGTIRRRIMKGASDRVVAPSN

>RXN01002 TRANSLATE of: rxn01002.seq check: 1757 from: 1 to: 804
 MNSDASATTNSWAINFDHVSVTYPNGTKALDDVSLTINPGEMVAIVGLSGSGKSTLIRTI
 NGLVRATEGTVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSSRSVFQNVLVGRFAHT
 AWWRNLLGFPTHEHDQIAFAHALESVGILHKVWTRAGALSGGQKQORVAIARALSQDPSVML
 ADEPVASLDPPTAHSMVRDLENINNVEGLTVLVNLHLIDLARQYTTTLVGLRAGKLVDYD
 PISEATDKDFEAIYGRPIQAKDLLGDRA

>RXN01141 TRANSLATE of: rxn01141.seq check: 9956 from: 1 to: 825
 LSTALAGAARYVTSTSNNEPADNTPLTIGYVPIAGSAPIAIADALGLFKKHGVNVTLLKKY
 SGWSDLWTAYATEQLDVAHMLSPMTVAINAGVTNASRPTLSFTQNTNGQAITLASKHYG
 SVNSAADLKGMLVGIPFEYSVHALLLRDYLVSNVADPIADLELRLLRPADMVAQLTVEGI
 DGFIGPGPFNERAISNGSGRIWLLTKQLWDKHPCCAVAMAKEWKAEHPTAAQGVNLALKEE
 ASAILSNPAQFDSSARTLSQEKYLNQPATLLDGPS

>RXN01142 TRANSLATE of: rxn01142.seq check: 3960 from: 1 to: 498
 LTARGNIDFGLRSARPSLSKTERADITRTHLEQVGLTDAAERRPARLSGGMQQRVGIARA
 FAIDPPIMLLDEPFGALDALTRRELQLQLLNIWEASRRTVVMVTHDVDEAILLSDRVLM
 SKSPEATIITDIPVNLPRPRHELSSEDASVEAETTALRKRMHLHLEH

>RXN01164 TRANSLATE of: rxn01164.seq check: 868 from: 1 to: 1635

VTLEFVRLALAAVGGLEFVFASNEPIGWFWAGIVGTALFFISLAPWDLGVPQKRRKKNEPVP
 FLOQMSTGPTVTVQGMLLGFVHGLVTVLQLLPWIGEFVGSLLPYVALSVVEALYSIALGAFG
 VLIARWRDVKVLLFPAMYVAVEYLRSSWPFDFGFAWVRLAWGQINGPLANLALGGVAFVT
 FSTVLAAVGVAMVLIISKKRLAGAIITASVIAIGAVSSLYVDRNGTSDESIEVAAIQGNVP
 RMGLDFNAQRRAVLANHARETLKLDEQVDLVIWPENSSDVNPFSDAQARAIIDGAVEHVQ
 APILVGTITVDEVGPRNTMQVFDPEGAEEYHNKKFLQPFGEYMPFREFLRIFSPYVDSA
 GNFQPGDGTGVVEMNAANLGRAVTVGVMTCYEVIFDRAGRDAIANGAEFLTTPNNATFG
 FTDMTYQQLAMSRMRAIEFDRAVVVAATSGVSAIVNPDGSIQNTRIFEAATLTESIPLK
 DTVTIAARVGFYVELLLVIIGVLAGLFAIRMNSRSKSAKGSARPAQVRVKKVPAKKAATN
 RRKVK

>RXN01168 TRANSLATE of: rxn01168.seq check: 6703 from: 1 to: 810
 MSSEAVDATTLVLIPTYNELNPLIVDRVRTATPDVHVLIVDDNSPDGTGERADKLAAD
 DDHIFVLHREGKGGGLCAEYMAGFQWGLERDYQVLCEMDADGSHAPEQLHLLLAETNGAD
 LVIGSRYVPGGRVNWPKNRWLLSKGGNVYISVALGAGLTDMTAGYRAFRREVLEALPLD
 ELSNAGYIFQVEIAYRAVEAGFDVREVPITFTEREIGESKLDGSFVKDSLLEVTKWGLKH
 RGGQAKELSKEMVGLLNYEWKHFKKRNTWL

>RXN01285 TRANSLATE of: rxn01285.seq check: 1049 from: 1 to: 726
 LNVITPDNTFTAIIGPNGCGKSTLLRGFSRVLNPHQHGKVLLDGRQLDSFKPKIEIARELGL
 LPQTSIAPEGIRVYDLIARGRAPYQSLIQQWRTSDEDAVAQALASTNLTELAARLVDELS
 GGQRQRVVWVAMLLAQQTPIMLLDEPTTFLDTAHQYELLELLRAFNEAGKTVVTVLHDLNQ
 AARYADHLIVMKDGHVHATGTPEEVLTAEMVQGVFGLPCIISPDPVTGTPTVVPLSRRA
 GA

>RXN01298 TRANSLATE of: rxn01298.seq check: 8940 from: 1 to: 930
 VSTLISEPEVDKLRKRAKRSRTEWWLAAALLAPNLLLLAIFTYRPLLDNFRLSFFNWN
 SSPTSTFIGFDNYVEFFTRSDTLQVVLNTVIFTACAVIGSMVLGLLLAMLLDQKLFGRNF
 VRSMVFAPFVISGAAIGVAFQFVFDPNFGLVQDLLGRIGVDSPOFYQNPWALFMVTFTF
 VWKNLGYSEFVIYLAALQGLNKDLSEAPVDGASAWTRFWKVTLPLQLRPTTFFLSITVTLN
 SVQVFDIIHTMTRGGPLGNGTTTLVYQVYTETFTNYRAGYGATITILFLLLLIITVIQV
 RYMDKENKQK

>RXN01323 TRANSLATE of: rxn01323.seq check: 658 from: 1 to: 2265
 MAQTPAKIPAAALNFIDVDLGVGTGMTCTSCSARVERKLNKLDGVEATVNYATESAQVSYDP
 SKVSPEQLIKTVEDTGYGAFTMASAAAESEEDNAPADSGQSRIDAARDHEAADLKHVIV
 SALLSVPVVLVSMIPALQFNWQWAVLTLVTPIFFWGGSPFHKATWANLKRGSFTMNTLV
 SLGTSAADLWSLWALFIENAGHPGKMEMHLLPSASTMDEIYLETVAVVITFLLLGRWFE
 TKAKGQSEALRKLLDMGAKDAVVLRDGAEVVPVNLKLGDFVITRPGEKIATDGEVDE
 GSSAVDESMLTGESIPVEVTKGSKVTGATLNTSGRLMVKVTRIGADTTLSQMAKLVTDQ
 SKKAPVQRLVDQISQVFVPVVIIVIAIATLIAHLVFTDAGLAPAFTAATAVAVLIIACPCALG
 LATPTALLVGTGRGAQLGLLIKGPETILESTKKVDTIVLDKTGTVTGTMSVTDVTAINYS
 ETEILEFAAAVESASEHPAQAIAKAAEHEQVTDFQNTAGQEVTVGVVGRGHEVRVGRPSST
 LIDALLHPFQHAQKIGGTPVVVTIDGVDSGIITVRDVTVKDTSAEATIRGLKELGLTPILLT
 GDNEGAAKSVAEEVGIDQVIANVLPHEKVQNVLEALQAQGNVAMVGDGVNDAAALAQADL
 GLAMGAGTDVAIEASDITLMNNDLRSVDAIRLSRKTTLGTIKGNLFWAFAYNVALIPVAA
 IGLLNPMLAGIAMAFSSVFVVSNSLRRLRGFKARSN

>RXN01338 TRANSLATE of: rxn01338.seq check: 9102 from: 1 to: 1902
 KTYTPNPWMLFIRSFDTGIIITVAALVAIAIHLILWLALDLGLAKNWPLIAIVIVGGIPLM
 WDLVLSAIKTRGGADTLAAVSIITSVLLGEWLVAIIIVLMLSGGEALEEASRRASGTL
 ALARRAPSTAHRLLGATILDGTEEIAVEEITVGDLVAVLPHELCPVDGEIVAGHGTMDES
 YLTGEPYVVSXSKGSQAMSGAVNGDTPLTIVATKLAHDSRYAQIVGVLHEAENNRPEMRR
 MADRLGAWYTVIALALGGLGWIVSGDPVRFLAVVVVATPCPLLIAPVVAIIGATISLAARR
 GIIIVKNPGLMENASGVKTMFDTGTLTGRPVITDIHTAPGVEEDTVLALAASVERYSR
 HPLADAIREGAKRELHLPDVVEVSESRPGQGLTGTVGEHLVRITNRRSTLEIDPDSKNYI
 PVTSSGMEVVLVDKYAALIRLRDEPRASASEFIAHLPPKKHKVVDKLMIIISGDRASEVRY
 LADKVGIDEVHAEASPEDKLNIVNRHNEHGATMFLGDGINDAPAMAVATVGVAMGADSDV
 TSEAADAVILDSSLERLDDLLHISARMRRIALQSAGGGMALSVIGMILAVFGFLTPLMGA
 IFQEVIDVLAILNSARVALPRGAISDFDTQEKVS

>RXN01411 TRANSLATE of: rxn01411.seq check: 3735 from: 1 to: 765
 MLGVGWRIFFLMAVPLGLIGWWIRTGAQENVRPASERPEAPIKQALRTEWKMMMLRVGGFI
 SCTGLSFYIFTTYMTTFLRSTVGLGTLVLAGNIIALSMAAIVAPFVGRAIDKFPRRNIM
 AFATLSTVIMAI PAYIIAGQGTLTASLIAQVMLGIGAVTANCVTSVMMAEVFQEVTRGTS
 AGITYNVTYAIFGGSAPFISTALVSWTGSPLAPAVYMIIALFAFTASRFIPETSPVFVT
 ATPAIKAPKVLVNP

>RXN01808 TRANSLATE of: rxn01808.seq check: 4151 from: 1 to: 1149
 QSLACKELAWMRGGAPARTSKPGFRLEAAEALIAEVPAPRDKVELMAFSKSRQGRVIEL
 EDATVATPDDRILVEDLTWRLAPGERIGLVGVNGSGKTTLLRTLAGEQPLQAGKRIEGQT
 VKLGWLRQELDDLDLSRRLIDCEDVASVMMGDKQVSASQLAERLGFSPKRQRTFPVGD
 SGGERRRLQLTRVLMAPENVLLLDDEPTNDLDIDTLQELSLLDGWPGTMVVISHDRYLIE
 RVTDSWALFEGDGKLTNLPGGIEEYLQRRAMAAAEDSGVLNLGAATQAGTFSATEQAA
 TSVESSGISSQERHRTKEMNALERKMGLDQQMDKLNQQLADAAEAMDTIKLTELDTKL
 RAVQEEHGELEMQLWLELGEIEG

>RXN01939 TRANSLATE of: rxn01939.seq check: 574 from: 1 to: 1731
 MTTNIPQTPNHEGEQPLLELKDLKISFTSSTGVVDAVRGANLTIYPGQSVIAIVGESGSGK
 STTAMSIIGLLPGTGKVTESIMFDGQDITGLSNKQMEKYRGSEIGLVPQDPMTNLNPVW
 RIGTQVKESLRANHVVPVPGSEMDKRVAEVLAEAGLPDAERRAKQYPHEFSGGMRQALIAI
 GLAARPKLLIADDEPTSDLDVTQRIQILDHLETITKDLGTAVLFITHDLGLAERAHLV
 MHRGRIVESGPSLKILRNPHYPYTQRLVKAAPSLASARIQSAEQGIESAELLSATAVAE
 GTIPEMEEKVIEVKNLTREFDIRGARGDKKKLKAVDVVSFFVRKGTTLVGESGSGKST
 VANMVLNLLIPTSGEVLYNGTDLTSLSHKEIFQMRRLQVVFQNPYGSIDPMYSIYRCIE
 EPLTIHKVGGDRKAREARVAELLDVSMRSTMRYPNELSGGQRQRIAIARALALNPEV
 IVLDEAVSALDVLVQNQILTLAELQQLKLTLYLFITHDLAVVRQTADDVVMQKGRIVE
 KGRTDDIFNDPQQHYTRDLINAVPGLGIELGTGENLV

>RXN01995 TRANSLATE of: rxn01995.seq check: 3763 from: 1 to: 1338
 MDIRQTINDTAMSRQWFIVFIAVLLNALDGFVLAAMSFTANAVTEEFGLSGSQLGVLLS
 SALFGMTAGSLLFGPIGDRFGRKNALMIALLFNVVGLVLSATAQSAGQLGVWRLITGIGI
 GGILACITVVISSEFSNNKNRGMAMSIYAAGYGIGASLGGFGAAQLIPTFGWRSVFAAGAI
 ATGIATITATFFFLPESVDWLSTRPAGARDKINYIARRLGKVGTFELPGEQSLSTKKAGL
 QSYAVLVNKENRGTSIKLWVAFGIVMFGFYFANTWTPKLLVETGMSEQQGIIGGLMLSMG
 GAFGSLLYGFLTTFKSSRNTLMTFMVLSGLTLILFISSTSVPSTAFASGVVVGMLINGCV
 AGLYTLSPQLYSAEVRTTGVGAAIGMRVGAISAPLLVGGLLDGWSPTQLYGVAVIVI
 AGATALIGMRTQAVAVEKQPEALATK

>RXN02062 TRANSLATE of: rxn02062.seq check: 5414 from: 1 to: 1170
 MRVGMMTREYPPEVYGGAGVHVTELTRFMREIAEVDVHCMGAPRDMEGVFVHGVDPALES
 ANPAIKTLSTGLRMAEAANNVDVHSHSTWYAGLGHLAARLHGIPHVATAHSLEPDRPWK
 REQLGGGYDVSSWSEKNAMEYADAVIAVSARMKDSILAAYPRIEPDNVRVVLNGIDTELW
 QPRPTFDDAEDSVLRSLGVDPQRPIVAFVGRITRQKGVHEHLIKAAALFDESQVLVLCAGA
 PDTPEIAARTTALVEELQAKREGIFWVQDMLGKDKIQEILTAADTFVCPSTIYEPLGIVNL
 EAMACNTAVVASDVGGIPEVVVDGTTGALVHYDENDVETFERDIAEAVNKMVADRETAAK
 FGLAGRERAINDFSWATIAQQTIDVYKSLM

>RXN02096 TRANSLATE of: rxn02096.seq check: 3261 from: 1 to: 1692
 MGLDVSDEQIEHAARLAQAHDIFIDRLPNKYEEVIGERGLTSLGGQRQRIALARAFLAHPK
 VLVLDATSAIDASTEDRIFQALREELHDVTILIIAHRHSTLELGDRVGLVEDGRVTALG
 PLSEMRDHARFSLMALDFQDSDHPEFTLDNGSLPSQEQLWPEVSTEKQYKILAPAPGRG
 RGMSMPATPELLAQIEALPAATEETRVDAGRRTSTSGFKLLSLFKQVRWLVAVIALLL
 VGVAADLAFPTLMRAAIDNGVQAQSTSTLWWIAIAGSVVVLWSWAAAAINTIITARTGER
 LLYGLRLRSFVHLLRLSMSYFERTMSGRIMTRMTTIDIDNLSSFLQSGLAQTVVSVGTIG
 VVTMLAITDAQALVALSVVPIIIVLTILFRRISSRLYTASREQASQVNAVHESIAGLR
 TAQMHRMEDQVFDNYAGEAEFRRLRVKSQTAIAIYFPLGALSEIAQALVLGFGALQVT
 RGDISTGVLVAFVLYMGLMFGPIQQLSQIFDSYQQAAGVFRRITELLATQPSVQIWAPTG
 TLGRLPRSLYCLTTSPSAIQTIRS

>RXN02348 TRANSLATE of: rxn02348.seq check: 8038 from: 1 to: 1884
 MLNRMKSARPKSVAPKSGQALLTLGALGVVFGDIGTSPLYSLHTAFSMQHKNKVEVTQENV

YGIISMVLWTITLIVTVKYVMLVTRADNQGGGILALVALLKNRGHWGKFVAVAGMLGAA
LFYGDVVITPAISVLSATEGLTVISPSFERFILPVSLAVLIAIFAIQPLGTEKVGKAFGP
IMLLWFVTLAAGLIPQIIGHPEILQSLSPHWALRLIVAEPFQAFVLLGAVVLTVTGAEL
YADMGHFGARPIRVAWFCVVMPALILTYLGQGALVINQPEAVRNPMFYLAPEGLRIPLVI
LATIATVIASQAVISGAYSLTKQAVNLKLLPRMVIRHTSRKEEGQIYMPLVNGLLFVSVM
VVVLVFRSSESLASAYGLAVTGTLVLVSVLYLIYVHTTWWKTALFIVLIGIPEVLLFASN
TTKIHGGWLPPLIAAVLIVVMRTWEWGS DRVNQERAELELPMDKFLEKLDQPHNIGLRK
VAEVAVFPHGTSDTVPLSLVRCVKDLKLLYREIVIVRIVQEHVPHVPPEERAEMEVLHHA
PIRVVRVDLHLGYFDEQNLPEHLHAIDPTWDNATYFLSALTLSRSLPGKIAGWRDRLYLS
MERNQASRTESFKLQPSKITVTGTELHL

>RXN02354 TRANSLATE of: rxn02354.seq check: 8723 from: 1 to: 834
MTKRTKGLILNYAGVVFILFWGLAPFYWMVITALRDSKHTFDTFWPTHVTLDNFRDALA
TDKGNFLAAIGNSLVISVTTTIAIVLVGVFTAYALARLEFPKGKIVTGIIAASMFPGI
ALVTPLFQIFGDLNWIGTYQALIIPNISFALPLTIYTLVSFFRQLPWELEESARVDGATR
GQAFRMILLPLAAPALFTTAILAFIATWNEFMLARQLSNTSTEPVTVAIARFTGPSSFEY
PYASVMAAGALVTIPLIIMVLIFQRRIVSGLTAGGVKA

>RXN02356 TRANSLATE of: rxn02356.seq check: 7192 from: 1 to: 996
MATVTFDKVTIRYPGAERATVHELDLDIADGEFLVLVGPSCGKSTTLRALAGLEGVESG
VIKIDGKDVGTQEPADRDIA MVFQNYALYPHMTVAKNMGFALKLAKLPQAQIDAKVNEAA
EILGLTEFLDRKPKDLSSGQRQVRAMGRALVRDPKVFLMDEPLSNLDAKLRVQTRAEVAA
LQRRLGTTTVYVTHDQVEAMTMGDRVAVLKDGLLQQVAPPRELYDAPVNEFVAGFIGSPS
MNLFPANGHKMGVRPEKMLVNETPEGFTSIDAVVDIVEELGSESYVYATWEGHRLVARWV
EGPVPAPGTFVTFSDAAQAHFDESGERIA

>RXN02391 TRANSLATE of: rxn02391.seq check: 7541 from: 1 to: 399
MTQSDLPDDVQELVTKIFGLARDGGAESAATLGAYVDNGVDVNLNSQDGNLTLLMLAAYAG
HADVVQALIERGADVDRVNNRNQTPLAGAI FKKEEAVIEALLAGGADPYAGTPTAVDTAK
MFGREDLVARFES

>RXN02442 TRANSLATE of: rxn02442.seq check: 5164 from: 1 to: 849
MKFFTDALIVPFDVSFISRALVAGCLAAILCSLIGTWVILRRLTFFGDAMSHGLLPGVAT
ASLLGGNLMFGAAISALIMSAGVVWTSRKSSLSQDVSIGLQFITMLSLGVVIVSHSDSHA
VDLTSFLEGDILGVRPSDIFI IAIATVLGGTLTIFLFHRQFTALAFDERKAHTLGLNPRFA
HLLMLALIALATVVSFQVVGTTLLVFGLLIGPPATAALLVQDKASISLIMIVASLLGCAEI
YLGLLISWHASTAAGATITLLSAAIFFATLLTKSAISRLNFTA

>RXN02447 TRANSLATE of: rxn02447.seq check: 8454 from: 1 to: 1095
TVVPVYLAELAPLEIRGSLTGRNELAIVTGQLLAFVINALIAVTLHGVIDGIWRIMFAVC
ALPAVALFLGMLRMPESPRWLVNQGRYDDARRVMETVRTPERAKAEMDEIIAVHSENNAA
LPGVKQSSGQASGVSSKHTHMSIGEVLSNKWLVRLLIAGIGVAVAQQLTGINAIMYYGT
RVLEESGMSAEMAVVANIAFGAVAVIGGLIALRNMDRDRRTTFIIGLSLTTFHLLIAA
AGTLLPEGNSIRPFAIMILVVGFLSMQTFNLVAVVWVLAEIFPVRMKGIGTGISVFCGW
GINGVLALFFPALVSGVGITFSFLIFAVVGVI ALAFVTKFVPETRGRSLEELDHAFTGQ
IFKKA

>RXN02455 TRANSLATE of: rxn02455.seq check: 2559 from: 1 to: 1269
LKRLTRIASISMASMLAAASLVACSGSTDEEGDVYFLNFKPEQDVAYQEIAKAYTEETGV
KVKVVTAAAGSYEQTLKAEIGKDEAPTLFQVNGPAGFITWQDYMADMSDTEVAKQLTDDI
PPLTTEDGEVRGVPPFAVEGFGIINDEIFDKYIATSGAKIKSTDEITSYQKLKEVAEDMQ
AKKDELGIEGAFASSTLSSEDWRWQTHLANAPIWQEYQDKGVEDTNEIEFSYNKEYKNL
FDLYLENSTVEKSLAPSKTVSDSMAEFAQGKAAMVQNGNVAWSQISETSGNVVKEDKIKF
LPMYMGLPDEEKHGINVG TENYLVGNSEASEVDQATKDFVDWLFTSEAGKEHVVKDLGF
IAPFESYTAENTPNDPLSEQVAEAIANKDLTTYPNWFQYFSPQOFKDDFGQDLSQYASGK
LKW

>RXN02515 TRANSLATE of: rxn02515.seq check: 4857 from: 1 to: 756
MSTLEIRNLHAQVLPSDESAEPKEILKGVNLTINSGEIHAIMGPNGSGKSTLAYTLGGHP
RYEVTAGEVLLDGENILEMEVDERARAGLFLAMQYPTIIPGVSVANFLRSAATAIRGEAP
KLREWVKEVRTAQEALAI DPEFSNRSVNEGFSGGEKKRHEVLQLDLLKPKFAIMDETDSG

LDVDALRIVSEGINSYKQETEGGILMITHYKRILNYVKPDFIHVFANGQIVTTGGAELAD
KLEADGYDQFIK

>RXN02549 TRANSLATE of: rxn02549.seq check: 8075 from: 1 to: 2703
MVHAKQTKKPLPRFLHSAHFYVWIVLGFVVFQAQPYGQVAADTKLDLLLNPAAGFLTALHA
WTDFTLGLQQLNQAYGYLFPQGGFFLITDFLPDWIAQRLWWVLVLGLGFSGFYALVARLG
IGNPAFRVIAALLFALSPTTLTTLTAISSETWPIMLAPWVCLPLLSRNVDARAIALSLLP
AACMGAVNATATMAALI PAALILLYRGLFLRLLLLWGMGVLAVNSWWIGPLLVLGKYAPPF
TEFIESSSVTTSWLNVPVEILRGTTSWTPFVDTERQAGYLLVNDALFVTL SVLVAALGLIG
LTLMKHRGLWAFMLAIGLLILGSAHLTAVQEFLDGPGAALRNHFKFDLLVRMPLMVGVAA
LGSHISLPLLGTTALTSGQGKHHTIPLPLQKRQAAGLLVVI IAVGALAPAWSARLLPQGT
WDEVPDYWEATEFLNQATGTRTLIWPSPPFARQDWGWRDEPAQPLLDVWPWAVRDAIP
LVPPEAIRGLDGLDDLGTGLTGLNDEALKRLGIGAVLVRHDLEADPDIEVDLPGEKHTFG
SQGQVDVYLTDPDRNMWITSGTSKQLPTVAGGGEILSLLDTINGYSPRTLVSENAQIVTD
TPQLVGNTYGDGTSSAALASLDETEVKNRIVDYPASAGPMTQVVQEGSITASSSGSDATSF
GGADPDRSLNSLLDHRNTAWYPTPGDTSPWLEVSGTGTTLSISPRSTVTATITSGDSVM
VREFEKGRTTTTVTLAEPERIEFDGFGVISELSLEGLSRTITVPETSPDVQQFVFQRLTV
PTSFLDRTFTVPRHMSVTVEAQSCVTELDGDRIDCGPSNSPPEPTRCAPNRNGSPSPNP
LRSPLESQQQTSRQHPPTACSSPRALSIQVPARLSTPPPPFQSNSTPPPKVSSSPRTPPA
S

>RXN02570 TRANSLATE of: rxn02570.seq check: 2673 from: 1 to: 642
MNPLTWIIGAFSMWIVVLGVNKLGLSIAVIIIAQVVMIRVRNVSVLASTALLSVPALAS
MALIHMPYSSDGWLIALTLTARFSALMSIFLLAATAITIPELVKSLYRWPKLAYIVGSAL
QMIPQGGKQTLALVRDANALGRSVKGPVRAVKYVGLPLITHLLSAGAARAIPLEVAGLDR
PGPRTVLVEVVEGRVEKHCRWLLPLLAVGMAWWL

>RXN02595 TRANSLATE of: rxn02595.seq check: 5016 from: 1 to: 1164
VIVVAMASIMACLKAAARLNNPMKILLLCWRDTHHPQGGGSERYLERVGEFLADQGHEVVF
RTAGHTDAPRRSFRDGVYRSRGGKFSVYPKAWVAMMLGRVIGIGTFKVDVVVDQTONGIP
FFGKFFSGKPTVLLTHHCHKEQWPVVGRVLAKVGWLIIESQIAPRAYKTAPYVTVSEPSAE
ELIALGVDDQRIHIVRNGVDPVPLHTPKLDRDQGHAVTSLRLVPHKQIEHAMDVVAALDG
VVLDDVESGWWQKELVDYARTLGVS DRVVFHGGQVAEDHKHALLERATIHLMPSRKEGWGL
AVTEAAQHGVPTIGYRSSGGLRDSVVDGETGLLVDSKAELISATKTLIDASLRSKLGAS
AKQRAENYKWDTAGAQFEELLLGLASKK

>RXN02614 TRANSLATE of: rxn02614.seq check: 5216 from: 1 to: 729
MTATLSLKPAATVRGLRKS YGTEKVLQIDLTINCGEVTALIGRSGSGKSTILRVLAGLS
KEHSGSVEISGNPAVAFQEPRLLPWKTVDNVTFGNRTDISWSEAQERASALLAEVKLP
DSDAAWPLTSLGGQAQRVSLARALISEPELLLLDEPFGALDALTRLTAQDLLLLKTVNTRN
LGVLLVTHDVSEAIADHVLDDGAIHSLTVDIPGDRRTHPSFASYTAQLLEWLEIT
TPA

>RXN02795 TRANSLATE of: rxn02795.seq check: 7318 from: 1 to: 1437
VLKVS DLTVGNNFVHNVSFEVNPGERVGIIGESGSGKSLTALSIMGLTDLP TTGQITFNG
KPSATFRGTRIAMVFQEPMSALNPLMRIGRQIEEMMTLHGASKKDARARLKSLLIDVSLP
ERTASAYPHELSSGGQRQALIAMALANDPDLICDEPTTALDVVVQKQIVDLLLLRLTKER
GTALLFITHDLGLIARTCERLLVMKSGETVERGDTEAILRSPAHSYTOQLLDASILDQPE
IASDSGAPVVIDVEEASKSFKETTALHKVSLAVRKGDLGIVGGSGSGKTTLKLIAGLD
KPTTGTVAVTGGVQMVFDQPQSSLNPRMKIKDIVAEPLLGWNAAEKTRVAEVITQVGLS
PDVLD RYPHEFSGGQRQRI SIARALAIKPAILLADEPVSALDVSVRKQVLDLLQQLVEEY
GITLVFVSHDLAVVRHLCTTVWVMEQGRVLEQGPIDSVYDHPQTEYTKELLDAVPRLSL

>RXN02925 TRANSLATE of: rxn02925.seq check: 5237 from: 1 to: 2217
MSTPHHHGDHPAPETDHTHHPNHAGHEHHADAATHGQAMPDHPHSTVDEEHQVHSHGEH
AGHSAAMFRDRFWWSLILSVPVVFFSPMFADLLGYNIPEIPGAYWIPPVLGTIIFLYGGT
PFLKGAMTELKSRQPGMMLLIAMAITVAFIASWVTTLGLGGFHLDFWWELALLVTIMLLG
HWLEMALGAASSALDALAALLPDEAEKVVDGTTTRTVAISELAVDDVVLVRAGARVPADG
TIIDGAAEFDEAMITGESRPVYRDTGETVVAGTVATDNTVRIRVEATGGDTALAGIQRMV
ADAQASSSRAQALADRAAALLFWFALITALITAVVWTIIGSPDDAVVRAVTVLIACPHA
LGLAIPLVIAISSERAASKSVLIKDRMALEHMRTIDVVLFDKTGTLTEGAHAVTGVPAT

GIAEGELLALAAAAEADSEHPVARAIVTAAAAHPEASQRQLRATGFTAASGRGIRATVDG
 AEILVGGPNMLREFNLTPGELADITGSWAQRGAGVLHVVRDGEIIGAVAVEDKIRPESR
 AAVRALQARGVKVAMITGDATQVAQAVGKDLGIDEVFAEVLPPQDKDTKVTQLQERGLSVA
 MVGDGVNDAPALARAIEVGIAIGAGTDVAMESAGVVLASDDPRAVLSMIELSHASYRKMVQ
 NLVWATGYNIVAVPLAAGVLAPIGVLLPPAAAAAILMSLSTIIVALNAQLLRRIDLDPAHL
 APTDGKEEKAHVSSAAPVR

>RXN02933 TRANSLATE of: rxn02933.seq check: 4913 from: 1 to: 810
 MPLSGKIGGFIVAVFVLAALSFIWTFDPVQAFPQERLEGSSLRHLLGTDTRYGRDVLSSQ
 IMVGSRVTLVLVGIIAIAAALIGTPLGIAAGMRRGMVETFFVMRGADLMLAFPALLLAIIS
 GAVFGASTWSAMVAIGIAGIPSFARVARAGTLQVTSQDFIAAARLSKVSSARIALRHILP
 NITSMLIVQASVAFALAILAEALSFLGLGTLTPDPSPWGRMLQTAQASIGVTPMLAVWPG
 AAIALTVLGFENLFGDGLRDAIDPKREVGRA

>RXN02945 TRANSLATE of: rxn02945.seq check: 2147 from: 1 to: 933
 MTTALGTRVVARNFGRHASRENPAKLDINFEIAPGERILLTGASGAGKSTLLAALAGVL
 GGSDEGVSTGELLVDAPSIGLVLPQDPSQVIASRIGDDVAFGCENLQIPREEIWPRVERA
 LELVGLDLPLSHPTKYLSSGGQKQRLALAGVIAMGARLILLDEPTANLDPQGGQKNVVAVD
 RVVQETGATLIVVEHRHELWVNIIDRIISITDGEDVQPAELIKVGQLPGAQPSTSKPILW
 ANDLLCTWGGRLRSFEVPEGASTVITGPNAGKSTLALTMGGLLPRKVGSWNSLTRCAAL
 TRPRTSGVQLI

>RXN02975 TRANSLATE of: rxn02975.seq check: 5313 from: 1 to: 249
 VIVTNDLEVRVGARTLLDAPGQLLRVQPGDRIGLVGRNGAGKTTTMRILSGETKPYGGSV
 TTSGEIGYLPQDSREGNIEQTAR

>RXN02994 TRANSLATE of: rxn02994.seq check: 4127 from: 1 to: 723
 IKMTGVQKYFGDFHALTDIDLEIPRGQVVVVLGSPSGSKSTLCRTINRLETIEEGTIEID
 GKVLPEEGKGLANLRADVGMVFQSFNLFPHLTIKDNVTLAPIKVRKMKKSEAEKLAMSL
 ERVGIANQADKYPAQLSGGQQQVVAIARALAMNPKIMLFDEPTSAIDPEMVNEVLDMAS
 LAKEGMTMVCVTHEMGFARKAADRVLFMADGLIVEDTEPDSFFTNPKSDRAKDFLGKILA
 H

>RXN03020 TRANSLATE of: rxn03020.seq check: 1931 from: 1 to: 603
 MTLHVSNNLNTVADGSTSRTLLNNIHFWMNSQAKSSVSPAHPAPENPPYSPSSAASKAPD
 SGTATLGDIDLLNPQNRAALRRNHLGIVFQQPNLLPSLTVLDDQLLLIPRLGRILPPSRSA
 RTQHKDKALSLNLSIGLGLDAKRKVSLESGGQQAQVNLARALMNSPKLLLVDEPTAALDQ
 HSASEVTELIVSMAHQYNAPT

>RXN03080 TRANSLATE of: rxn03080.seq check: 3725 from: 1 to: 780
 MPQLVEIRDNLNVEFPSPRHAVKNVSFSAPAGKVTALIGPNGAGKSTALSAIAGLVESTGEV
 MVGGSGVASKAKARARLLSLVPQNTLRLGFSARDVVAMGRYPHRRGFAVETDADRRAT
 DDALRAINALDIAEQPVNELSGGQQQLIHIGRALAQDTAVVLLDEPVSAIDLRHQVEVLQ
 LLRARANSGETTVIVVLHDLNHNHVARWCDHAVLMADGEVVSQGDIREVLEPATLSTVYGLPI
 AVRDDPETSSLRVIPHNP

>RXN03081 TRANSLATE of: rxn03081.seq check: 3848 from: 1 to: 459
 MKKSLIAIVASALVLSGCTSDSSDSSGTSGETVETTSITTSVAAADGAFPRVTLLDSSIT
 LESKPERIAVLTPEAASLVLPITGADRVVMTAEMDTADEETAALASQVEYQVKNNGRLDP
 EQVVAGDPDLVIVSARFDTEQGTIDILEGLNVP

>RXN03108 TRANSLATE of: rxn03108.seq check: 138 from: 1 to: 267
 MTKPNASVELNTITKSYGSTTIIGDTSITINDGEFVSLLDPSGCGKSTILKMIAGLASPS
 TGTVSAGNEEIKGPGPDRGMVFQDHALLP

>RXN03116 TRANSLATE of: rxn03116.seq check: 7423 from: 1 to: 609
 MGEVDVEKHFAFGLKAAKQRRFFARTVALMPQNPTIPAGLSVFDYVLLGRHPHSYAPGRA
 DDEIVKRCLADLKLEHFSRGLDELSSGGERQVSLARALAEPRIVLLDEPTSAIDIGHA
 QETLELIDAIRHRLGLTVIAAMHDLTLTAQYGDRLMMNGGRKVFEGTAAEVLTAAQRIS
 IYDATVIVEVIDGRPVVIPQRSH

>RXN03129 TRANSLATE of: rxn03129.seq check: 210 from: 1 to: 1224
 MASIVFENVTRKYSFGARPAVDKLNLEIADGEFLVLVGPSCGKSTSLRMLAGLEPIDEG
 RLLIDGKDATELRPQDRDIAMVFQSYALYPNMTVRDNMGFALKNQKVAEIEKRVAEAS
 RILQLDPYLDKPAALSGGQRQVRAMGRAIVREPSVFCMDEPLSNLDAKLRVSTRAEISG
 LQRRMGVTTVYVTHDQVEAMTMGDRVAVLLGLVQVQVDTFQNLVDYPANAFVASFIGSPS
 MNLEGTIRGDKVTLGTGIQISVPDEVAEEVRNNPDRFEGRPVIVGARPEHMYLTANES
 GAVLGEVSHIDELGADSMVYVLASGVKNPNTDLLGEGIPEDMRVTVVGAEETDKARLGIR
 VERHHGLKAGDKVHVVAAPKDVHLFDGLDGRRIGASVLAHAHTVQSGH

>RXN03164 TRANSLATE of: rxn03164.seq check: 9986 from: 1 to: 870
 MIYRRVGNISGLKLPALISLGLWHNFGDDKPLSTQRSIIHRAFDGRGVTHFDLANNYGPPAGS
 AETNFRGRLREDLKSHRDELISSKAGWDMWPGPYGFGGSRKYLVSLLDQSLTRLGLDYV
 DIFYHHRPDPDTPLEETMYALRDIVASGKALYVGISSYGPETAEAAEFMAEEGCPLLIH
 QPSYSIINRWVEEPPGDDGENLLQSAANNGLGVIAFSPLAQGLLTDKYLDGIPEGSRASQG
 KSLSEGMLNVNNIDMVRKLNLDIAQERGQSLAQMALAWVLREQREYGAGLP

>RXS00088 TRANSLATE OF: RXS00088.seq check: 1389 from: 1 to: 876
 IEDNHGTEGISLPIEGVAATDNRAFELLDWRGVELVAAPLQLVPFTVTGYTEEGGVANLGSHREPDLEA
 LAAAQPSLIINGQRFAQYYDDIIALNPDA TVVELDPRDGEPLDQELIRQAETLGEIFGEEEDA AKIVAD
 FESALERAKTAYAAISDQTVMAVNVSGGNIGYIAPSVGRTYGPIFDLVGLTPALEVGNASSDHEGDDIN
 VEAAIAANPDLLVMDRDGGTSTRNEADYVPAEQIVSDNEALANVKAVTDGYVYAPADTYTNENIITY
 TEILNGMADMFEKAAQ

>RXS00372 TRANSLATE OF: RXS00372.seq check: 2326 from: 1 to: 1077
 MSSKHPLKRTAVTVFALGASAAALVACSEPSDVTAEETTTASSSANASDAAGEKVTITVYTSEPEEKV
 DEINKAFMEANPDIEVEVYRAGTGDLTARIEAEKASGSI EADVLWAADAATFETYAAQGD LAELEDVET
 SDIIEEALDAENFYVGTRIPTVIAYNTEVVDQAE LPTSWADLTDPKYAGQLVMPDPAVSGAAAFNASV
 WKNDPALGEAWITALGENQPMIAQSNQPTSQEIAGGGHPVGIVVDYLVRLAAAGSPIDTIYASEGSPY
 ITEPAGVFADSEKKEAAERYINFLLSVEGQEI AVEQAYLPVREDVGTPEGTPELADIELMTPDLEVTA
 DKAAAVEFFQNAMN

>RXS00453 TRANSLATE OF: RXS00453.seq check: 3260 from: 1 to: 2349
 VISAWLLILAI VGGIALTMQKGFNSFTIEDTPSIDATVSLVENFPDQTNPVTAAGVNVVFQSP EGTTL
 DDPQMMTAMDAVVYIEDNLPDFGGGERFGNPVEVSPALEEMVIEQMTSMGLPEETA AKDAANLAVLSE
 DKTIGYTSFNIDVEAAEYVEQKHRDVINEAMQIGEDLGVRVEAGGPAFGDPIQIETTSEIIGIGIAFIV
 LIFTFGSLIAAGLPLITAVIGVGIGALAIVLATAFTDLNNVTPVLAVMIGLAVGIDYALFILSRYRAEY
 KRMPRADAAGMAVGTAGSAVVFAGATVIIALVALIIADIGFLTAMGISAAFTVFVAVLIALTFIPALLG
 VFGGHAFKGIPIGIGNPTPKQTWEQALNRRSKGRSWVKLVQKAPGLVAVVVLGLGALTIPAMNLQLS
 LPSDSTSNIDTTQRQSADLMAEGFGAGVNAPFLVIVDTHEVNADSTALQPLIEAQEP EEEGEFDREQAAR
 FATYMYVTQTYNSNIDVKNQAIISVNDDFTAAQILVTPYTG PADKETPELMHVLRAQEAQIEDVTGTTEL
 GTTGFTAVQLDITEQLEDAMPVYLAVVGLAIFLLILVFRSLLVPLVAGLGFLLSVGAAFGATVLVWQE
 GFGGFVNTPGPLISFMPIFLIGVTFGLAMDYQVFLVTRMREHYTHHNGKGQPGSKYTPVEQSVIEGFTQ
 GSRVVTAALIMIAVFVAFIDQPLPFIKIFGFALGAGVFFDAFFIRMGLVPASMFILMGKATWWMPKWL D
 RILPSLDIEGTALEKEWEEKQAAR

>RXS00479 TRANSLATE OF: RXS00479.seq check: 9191 from: 1 to: 2190
 MSTSITTENKKKSGPPRLMRIFLPALLILVWLVGAGVGGPYFGKVSEVSSNSQTTYLPESADATQVQEQ
 LGDFTDSESI PAIVVMVSDEPLTQQDITQLNEVVAGLSEL DIVSDEVSPAIPSEDGRAVQVFVPLNPSA
 ELTESVEKLSETLTQQTPDYVSTYVTGPAGFTADLSA AFAGIDGLLLAVALAAVLVILVIVYRSFILPI
 AVLATSLFALT VALLVWWLAKWDILLLSGQTQGILFILVIGAATDYSLLYVARFREELRVQQDKGIAT
 GKAIRASVEPILASGSTVIAGLLCLLFSDLKSNSTLGPVASVGII FAMLSALTLLPALLFVFGRAFWP
 KRPKYEPEKARAKNDIPASGIWSKVADLVEQHPRAIWVSTLIVLLLGA AFVPTLKADGVQSQDLVLGSS
 EARDGQQALGEHFPGGSGSPAYII VDETQAAQAADVVLNNDNFETVTVT SADSPSGSAPI TADGIVPLG
 SGTAPGPVVVEGQVLLQATLVEAPDSEEAQKAIRSIRQTFADENISAVVGGVTATSVDTNDASIHDRNL
 IIPIVLLVILVILMLLLRSIVAPLLLVTTVVSFATALGVAALLFNHVFSPFGADPAVPLYGFVFLVAL
 GIDYNIFLVTRIREETKTHGTRLGILRGLTVTGGVITSAGVLAATFAALYVIPILFLAQIAFIVA FGV
 LIDTLLVRAFLVPALFYDIGPKIWWPSKLSNQKYQKQPQL

>RXS00654 TRANSLATE OF: RXS00654.seq check: 6625 from: 1 to: 1266
 VLDILIYPVSGVMKLWHLHLLHNVA GLDDSLAWFFSLFGLVITIRAI IAPFTWQMYKSGRTAAHIRPHRA
 ALREEYKGYDEASIRELQKRQNDLNKEYGINPLAGCVPLGIQIPIVLGLYWALLRMARPEGLENPVF

QSIGFLTPEEVESFLAGRVSNVPLPAYVSMPTQLKYLSTTQAEVLSFVLPLFITAAILTAINMAMSMY
RSFQTN DYASGFSNGMLKFMIVMSILAPIFPLSLGLTGFPPTAIALYVWSNNLWTLTQTIIMMVILERK
YPLTDDDFKVHHELRDIYRAKQKEKRIFLWTRRKNRMLITPWNASTLHATNVELTKTRTAEINEAKQ
ARKEIANKRRETQREMNRAMQRLKQRRAEVKAKKKGLIDASPNETPSENEETKLSSPQVEPTTTAE
NREPSQED

>RXS00758 TRANSLATE OF: RXS00758.seq check: 161 from: 1 to: 1602
MTLKKSLAVTTAAALALSIAACSSDSSSSSSSSSSGSEGGDNVVLVNGTEPQNPLVPGNTNEVGGRIV
DSIFSGLVYYDVGSPVNDVAESIELEGDKTYRITIKDGQTFDTGTPVTAESFVNAWNNYNVANSTLSSY
FFESILGYEEGVESMEGLQVDDTTFTVELTQPESDPFLRLGYSAFFPLPESAFDDMDAFGENPIGNP
YKLQEWNNHNDATIVPNADYTGGROAQNNDGVKFIFYPTFDSAYADLLSDNLDVLDALPDSAFSSFEDEL
SGRSINQPSAVFQSFTIPESLEHFSGEEGVLRQAISLAVNRDEITQTIFEGTRTPATDFTSPVIDGHS
DSLQADVLTYDPERAQELWAQADEISPSWGEFSISYNADGGHQAWVDATANSIRNTLGIDAIGNPYPD
FKSLRDDVTNRTINGAFRTGWQADYPSLGNFLGPLYGTGAGSNDGDYSNPDFDAKLAEANAADVDAST
PLYNEAQEILLQDLPAIPTWYSNAVGGYSTNVNDNVEFQWNSQPAYYQITKN

>RXS00912 TRANSLATE OF: RXS00912.seq check: 8141 from: 1 to: 273
MDNTLYTAGLTIAAAFFMLSFIPTIYRIIVGPNSIDRLLGLDGTVMIQCSMATYICWTLDTTNTNFM
VIALLGFISSVSVARFRKRDGA

>RXS00932 TRANSLATE OF: RXS00932.seq check: 6704 from: 1 to: 474
MTPQKLHRRFAALLEMGTWTLIIIGMILKYSVTDVAVTPIAGGIHGFGLCFAAITITVWINNKWTFPQG
IAGLIVSVIPWAALPFALWADKKGLVAGGWRFSDPSEKPHFTFFDKILAQLVRHPIRSILILLVIIAVVF
SILLAMGPPYDPDAIANTVD

>RXS01346 TRANSLATE OF: RXS01346.seq check: 3214 from: 1 to: 1575
MRTATKVIATVMASLTALIGLASCSSSGTDPVNVSVNGTEPQRGLIPGDTNENGGRVDMLYSGLVY
FDEAGVAQNDLAASIDQETDTTYKITLRDGIKFSGSDITATDFVDTWNEFVENGLLNTSFFSPIKGYE
EGVETLEGLNVVDDRTFTIELAQPDSEFTQRIGYYGFAPMPASARDDIDAFGENPVSSGPYKLEQWDHN
AELKVVAHEHYDGPRAANNNDGLKYVFYAQNDAAYSDDLGNLDVLDLIPPSAYTTYEEELSGRSINQPA
ASYLELSIRMESPNFEGQQQLRRQAISMAINREEIAEQIFAGTYTPALDFTAPVLDGWRDDLNGNDVL
TFQPDKARELWEDAEEIAPFEGELQISYNADVPNREWVDAVANSISNELDVNATGNPFPDFKSFRD TYR
TTGLDGAYRTAWFADYPSIGNFLGPNYTSGVASNDAKYENPEFDQLIADAAAASTKEETFQAYAQAQEM
LLRDLPAIPLWYPNVVGGYSESVDNVSVNWKAIIPVYWAITKQ

>RXS01425 TRANSLATE OF: RXS01425.seq check: 9957 from: 1 to: 885
VLSPDSGITWALSIMFLTFTVRMVLVKPMVNTMRSQRKMQDMPAKMQAIREKYKNDQQKMEETRKLQK
EVGVNPIAGCLPMLVQIPVFLGLFHVLRFSFNRTGSGVGQLEMTVEQNANTPNYIFGVDEVQSFLRADLF
GAPLSSYITMPADAFDAFLGLDVSRLNIALVAAPMILIVVATHMNARLSVNRQEARKAAGKQQAASSD
QMAMQMOMMNKMLWFMPATILFTGFIWTIGLLVYMMSSNNVWTFQQRIFYAKMDAEEAEEEEKRAAK
RTTAPKPGVKPENPKKRKK

>RXS01658 TRANSLATE OF: RXS01658.seq check: 7999 from: 1 to: 1833
DPQILSPTFTQQQLRNFYGFDPQLAMDRFEVDGKLRDFVVAARELDENALQQNQDWINRHTVYTHGN
GFIAAQANQVDEVARDVGSTRGGYPVYTVSDLSNARAAESEDAAELGIKVDEPRVYGGPLIASATDGA
DYAIVGDTGDGPVEYD TDTSSYTYEGAGGV DIGNMVN RAMFALRYQEMNMLLSDRVGSSEKILFERDPR
SRVEKVAPWLTTDSKTYPTVIDGRIKWIVDGYTTLDSLPISTRTSLTEATQDAVMPDGTQPLITDRVG
YIRNSVKAVVDAYDGTVELYEFDTEDPVLKAWRGVFPD TVKDGSEISDELRAHLRYPEDLFKVQRDMLA
KYNVDDSGTFFTND AFWSVPGDPTAAEGRQELKQPPYVVAADPETGESSFQLITPFRGLQREYLSAHM
SASSDPVTYGEITVRVLPDTSVTQGPQAQDAMMSSDQVAQDQTLWRGSNDLHNGNLLTLPVGGGEILY
VEPIYSQRKDQASAFPKLLRVLVFYKGQVGYAPTIAEALSQVGIDPKEAQDIEEVDGTATTPSTDETD
DTDQPATETPTAPVSEAEGLAAINDALS NLEAARDSSFEYGRALDALDRAVD SYQSAQ

>RXS01677 TRANSLATE OF: RXS01677.seq check: 5194 from: 1 to: 744
VNQQSKKWLVP TLVVI IAVLLI AVLLMYRGNASDTAEGVSAAATSDSAAAATAASGSASGAADSDLTS
VEARDPSDPVAVGDVDAVGLVVFSDYQCPFCAKWSDETLPQMMKHVEDGNLRIEWREVNI FGEPSERG
ARAAYAAGLQDAYLEYHNALFANGEKPSDLLSEEGLIKLAGDLGLDESKFTADFQSPETAIAIAQHQQ
LGIDL GAYSTPAFL LGGPIMGAQPASVFEEAFAEQALAAKE

>RXS02586 TRANSLATE OF: RXS02586.seq check: 4914 from: 1 to: 270

MHLLRDDNNWAPGFVKKAYTVMGHGSEVEEAPRPTTTRRLNDDEEVTVEHAVVAGDTVASRGGGLSTQENR
DLVSFVELKARLEKRRLLEDLD

>RXS02587 TRANSLATE OF: RXS02587.seq check: 637 from: 1 to: 2091
VFSKWGHFAYRFRRIVPLVVIAAILALFVIFGTKLGDMSQEGWDDPGSSSTAAARIELETFGRDNDGD
VVLLFTAPEGTSFDDAEVSSISGYLDGLIENNPDEVSHINSYFDTRNQNLSSKDGQTFAALGLKGDG
EQTLKDFREIEDQLHPDNLAGGVTEVAGATAVADALDEGMAGDISRAEVFALPFVAILLLIVFGSVVA
AAMPLIVGILSILGSLGILAILAGFFQVNVFAQSVVTLGLGLAIDYGLFMVSRFREEMDKGTPVEQAV
ATTTATAGKTVVVFSAMVAVALSGLFVFPQAFLKSVAFGAISAVGLAALMSVTVLPSLFSMLGKNIDKW
SLRRTARTARRLEDTIWYRVPAMWRHAKAVTVGVVLLLLALTVPPLTGKFGGINETYLPANDTRVAQ
ERFDEAFPAFRTEPVKLVVTGADNNQLIDIYVQANEVEGLTDRFTAGATDDGTTVLSTGIQDRSLNEQ
VVEQLRAISVPEGVEVQIGGTPAMEIESIEALFEKLLWMALYIVLATFILMALVFGSVILPAKAIIMTI
LGMGATLGILTLMFVDGVGASALNFSPGPLMSPVLVLMALIIYGLSTDYEVFLVSRMVEARDKGESTDD
AIRYGTHTGSIITAAALIMIVVCGAFGFSEIVMMKYIAFGMIAALILDATIIIRMLLVPRRDAPASRRQ
LVGTRLR

>RXS02590 TRANSLATE OF: RXS02590.seq check: 3473 from: 1 to: 936
MGISLLSSLLKIHGFPVVADFFFALAVVVAIVIIIGWLIYRSPSFKTEVMPAWAMLSMGLIALGTASPV
VLGDDLWGFMFVCWSIGTAVGLVAYSLEYITAILRSKAGTPTFAWGLPLVTPMVASTAAQLHEHFELPA
MLWVSFGLFLLTLASAPAVFTRVYFYFYGPKAQGIPLMATPTSWIPLGMVGQSTAAQLIGASFGSKTA
ITMGIIYGIIMGIFTIPLGAIAHFVYFRAVFKGATYSPTWWASTFPVGTLSLGAHFLSQSTGVEWFNYF
SLYLIALMLFHVIVSTIAGTIAVMRRIVGKLKSQLA

>RXS02932 TRANSLATE OF: RXS02932.seq check: 938 from: 1 to: 972
VSKTEEGRSAAIIIIYAFPTFILLGAIIAFIFPEPFIPLTNYINIFLTIMFTMGLTLTVPDFQMVLKRP
LPILIGVVAQFVIMPFLAIVVAKMFNLNPALAVGLLMLGSPVPGGTSSNVIAFLARGDVALSVTMTSVST
IVSPIMTPFLMLLAGTETAVDGGGMATLVQTVLLPVIIGLVLRVFLNKWIDKILPILPYLSILGIGG
VVFAGAVAANAERLVSGLIVFVAVIVHNVLGYYVGYLTGRVFKFPEAANRTMAIEIGTQSAGLASGMAG
RFFTPEAALPGAVAALVHNITGAVYVGLVRNRPLTKASRKKEVAVSS

>RXS03042 TRANSLATE OF: RXS03042.seq check: 1569 from: 1 to: 606
LVLAFLVLLLVERSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLSFLPIMLIGLVFGL
AMDYQIFLVTRMREGFTKGKTAGNATSNGFKHGARVVTAAALIMVSVFAAFIAQDMAFIKTMGFALAVA
VFFDAFVVRMMIIPATMFLLDDKAWWLPKWLDKILPNVDVEGEGLSELHEARTEELKENVGVA

>RXS03075 TRANSLATE OF: RXS03075.seq check: 8649 from: 1 to: 726
VAKFLYKLGSTAYQKKWPFLAVWLIVILIGITTLAGLYAKPTSSSFIPGLDSVTTMEKMQERFPGSDDA
TSAPTGSVVIQAPGKTLTDPEVGAEVNQMLDEVTRATGVLKDADSVDVFLAAQGVAAQMTPALEAQGV
PAEKIAADIESISPLSADETTGIIISMTFDADSAMDISAEDREKVTNILDEYDDGDLTVVYNGNVFGAA
TSLDMTSELIGLLVAAVVLIVTFGSFIAAGMPLIS

>RXS03124 TRANSLATE OF: RXS03124.seq check: 3878 from: 1 to: 960
MTPTLASMIGLAVGIDYALFIVSRFRNELISQTGANDLEPKELAERLRTMPLAARAHAMGMAVGTAGSA
VVFAGTTVLIALVALSIINIPFLTVMAIAAAITVAIAVLVALSFLPALLGLLGTTRIFAARVPGPKVPDP
EDEKPTMGLKWVRLVRKMPVAYLLVGVVLLGAIAPATNMRLAMPTDGTSTLGTAPRTGYDMTADAFGP
GRNAPMIALIDATDVPEERPLVFGQAVEQFLNTDGVKNAQITQTTFENFDTAQILLPQNLMRMSAPLR
LSQLFVQMLRPSLMTPARRMALLASPQFTMTSLLASATSWFLTF

>RXS03125 TRANSLATE OF: RXS03125.seq check: 4701 from: 1 to: 171
LVLAFLVLLLVERSIWVPLIAALGFGLSVLATFGATVAIFQEGAFGIIDDPQPLLCF

>RXS03220 TRANSLATE OF: RXS03220.seq check: 3878 from: 1 to: 960
MGLREILSSKWLVRILLVGIGLVAQQLTGINSIMYYGVVLIIEAGFSENAALIANVAPGVIAVVGAFI
ALWMDGINRRTTLITGYSLTTISHVLIGIASVAFVPGDPLRPYVILTLVVVFEVGSMTFLNVATWVML
SELFPLAMRGFAIGISVFFLWIANAFGLFFPTIMEAVGLTGTFMFAGIGVVALIFIYTQVPETRGR
LEEIDEDVTSGVIFNKDIRKGVH

>RXS03221 TRANSLATE OF: RXS03221.seq check: 3878 from: 1 to: 960
MFRDPAPPSKGTTNLGDKMASTFIQADSPEKSKLPLTEGPYRKRLFYVALVATFGGLLFGYDTGVIN
GALNPMTRRELGLTAFTEGVVTSLLFGAAAGAMFFGRISDNWGRKTIISLAVAFFVGTMICVFAPSFA

VMVVGRVLLGLAVGGASTVVPVYLAELAPFEIRGSLAGRNELMIVVGQLAAFVINAIIGNVFGHHDGVW
RYMLATAAIPAIALFFG